

## FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCG  
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG  
CTGCTGCCGCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCT  
GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC  
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTGTCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC  
CAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGGCGACGGGTCTGCCGCTGCCACATGGGGTACCAGGGCCCGCTGTGCACCTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGCGGAGTGTGAAGTGGGCTGGGTGCT  
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACAGTGCAGAGAGTGTGACTCCAGCTGTGTG  
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCCTGTGTGAGGAAAAACG  
AAAACTGTACATACTCCAGGGAGCTACGTCTGTGTGTCTCCTGACGGCTTCGAAGAAACG  
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT  
GCCCTCCCGCAAGACCTGTAATGTGCCGGAATTACCCTTTAAATATTTCAGAAGGATGTCC  
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTTAAACAGCTGCATTTCTGGTTGTTCTTA  
AACAGACTGTATATTTTGATACAGTTCCTTGTAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGCGCCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA  
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG  
TGTGTCAATTAGGTGTGGAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLFLLLLLPAPAAKKPTPCHRCRLVDKFNQGMVDTAKKNFGGNTAWEEKTL SKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKT LKVVCSPGTYGPDCLACQGGSRPCSG  
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESKTCSGLTNRDCGCEVGVVLDE  
GACVDVDECAAEPFPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKEICISGYAREHGQCADVDECSLAETK  
CVRKNENCYNTPGSYVVCVPDGFEEEDACVPPAAEAEATEGESPTQLPSREDL

### **Signal peptide:**

amino acids 1-24

### **N-glycosylation sites.**

amino acids 190-194 and 251-255

### **Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

### **Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

### **Tyrosine kinase phosphorylation site.**

amino acids 303-310

### **N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

### **EGF-like domain cysteine pattern signature.**

amino acids 166-178

### **Leucine zipper pattern.**

amino acids 94-116

## FIGURE 3

CAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCGCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGAGCGCCAGCCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGCGCCCGGAGGAGCGCCTTC  
CTGCGCCGCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCTGCTGGCACTCGCGGCGGAGGC  
CGGCGCCGCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA  
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC  
CTGGCAAGCTCGAGGCGAGGCAGAATACTTCTATGAATTCCTGTCTTGGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA  
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGAAAAACAGGATGGGGTGGCAGCATTTGAAGT  
GGATGTGATTGTTATGAATTCGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT  
TCITTTAAACATGTCAACAAGCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTGTAAAT  
GAAAGACGCATCTGCGAGTGCTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG  
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCACTCTGCCACCTG  
GATTCATGGAGTGAACCTGTGACAAAACAACTGCTCAACCACCTGCTTTAATGGAGGGACC  
TGTTTCTACCTCGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAATCAG  
CAAATGCCACAACCTGTGCAAAATGGAGGTAATGCATTTGGTAAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT  
GGAACTGCGCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC  
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAACCTCCGACATCTGAACCGTTTAAAGTTACACCAAGTTTCATAGCCTTTGTTAACTTTCA  
TGTGTTGAATGTTCAAATAATGTTTATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT  
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTAAGTTTCTAAGTACGCTGTAG  
CATGATGGTATAGATTTTCTGTTTCACTGCTTTGGGACAGATTTTATATTATGTCAATTGA  
TCAGGTTAAAAATTTTCACTGTGTAGTTGGCAGATATTTCAAATTAACAATGCATTTATGGT  
GTCTGGGGGCGGGGAACATCAGAAAGGTTAAATTTGGGCAAAAATGCGTAAGTCAACAAGAT  
TTGGATGGTGAGTTAATGTTGAAGTTACAGCATTTCAGATTTTATTGTGAGATATTTAGAT  
GTTTGTACATTTTAAAAAATGCTCTTAATTTTAACTCTCAATACAATATATTTTGACC  
TTACCATTTTCCAGAGATTCAGTATTAACCAATGAATAGGGAATATAATGTATGAACCTTTTGCA  
TAAACAATATAATATTTCAAACACAATGAATAGGGAATATAATGTATGAACCTTTTGCA  
TTGGCTTGAAGCAATATAATATATTTGAACCAACACAGCTCTTACCTAATAAACATTTTAT  
ACTGTTTGTATGTATAAAAAAAGGTCGTCTTTAGTTTTTTGCAAAAAAAGGTCGTGCG  
CAATGAGGTCGTGCTCTTATGAGTTCGACCTGCAGAAGCTTGGC  
CGCATGAGGTCGTGCTCTTATGAGTTCGACCTGCAGAAGCTTGGC

## **FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPVC
EPGCGAGHTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

### **Signal peptide:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 88-92, 245-249

### **Casein kinase II phosphorylation site.**

amino acids 319-323

### **Tyrosine kinase phosphorylation site.**

amino acids 370-378

### **N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

### **EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGGGCCAGCCTGGG  
 CCCCAGCCACACCTTCCACAGGGGCCAGGAGCCACCATGTTGGCGATGTCCACTGGGGCTAC  
 TGCTGTTGCTGCGCGTGGCTGGCCACTTGGCTCTGGGTGCCACGAGGGTCTGTGGGCGCCGG  
 GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCGGGTACTGCCAGGA  
 GCAGGACCTGTGCTGCGCGGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT  
 GTTACTGTGACCTCTTCTGCAACCGCACGGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
 TGCCTCGGCGTGCCACCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCTGTATCTA  
 TCCAGTCTTGGGAACGTACTTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
 GGCATGTTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTTGGCAGGCTGG  
 GAACACACAGCGCTTCTGGGGCTTGACCTGGATTGAGGGCATTCTCATCCGCTGGGCACCA  
 TCCGCCCATCTTCTCGGTGATGAACATGCATGAAATTTATACAGTGTGTAACCCAGGGGAG  
 GTGCTTCCACAGCCCTTCGAGGCTCTGAGAAGTGGCCCAACCTGATTTCATGAGCCTCTTGA  
 CCAAGGCAACTGTGTCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
 CAATCCATTCTCTGGGACACATGACGCTGTCTCTGTCGCCCCAGAACCTGCTGTCTTGTGAC  
 ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCTGGTGGTTCTTGCCTGCG  
 CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACAGAGACGAGGCTGGCC  
 CTGCGCCCCCTGTATGATGACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC  
 CACTGCCCCAACGCTATGTTTAATAACAATGACATCTACAGTCACTCCTGTCTACCGCTT  
 CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
 TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
 CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
 AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC  
 CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC CGGCGTCAATGAGTGCGACATCGAG  
 AGCTTCGTGTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTTCATCACTGAGGCTG  
 CGGGCACACGCGGGGTCCGGCTGGGATCCAGGCTAAGGGCCGCGGGAAGAGGCCCAATG  
 GGGCGGTGACCCAGCCTCGCCGACAGAGCCCGGGCGCAGGGGGCGCCAGGGCGCTAAT  
 CCCGGCGGGGTTCCGCTGACGACGCGCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG  
 GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGACACAGCTGCAG  
 ATCCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
 CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG  
 TTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA  
 AGTGACCCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC  
 TAAATTTTGTATTTTTTTGTAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC  
 CCTGGGCTCAAGCGGTCCACCTGCCTCGCCTCCCAAAGTGCTGGGATGTCAGGCATGAGCC  
 ACTGCACCAGCCCTGTATTCTTATTCTTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA  
 TAAACCAAAAGTATTGATAAAAAAAA

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGGGCCAGCCTGGG

## **FIGURE 6**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223  
><subunit 1 of 1, 164 aa, 1 stop  
><MW: 18359, pI: 7.45, NX(S/T): 1  
MWRCPGLGLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC  
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPPFPIQGCMHGGRIYPVLGTYWDNCNR  
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

### **N-glycosylation site.**

amino acids 78-82, 161-165

### **Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

### **N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

### **Amidation site.**

amino acids 26-30, 318-322

### **Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

### FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCATTTCGTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCGCGGNTGGGCGTCTCGATGGTGCTGTGGTTCCTGCGTGCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTTCGGGGCAAGCGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATTGCGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTCTCTATAACGGGAGGACCTACAGCCACACGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATACCCGCGCATGGGACCCACTCAG

## FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAAGTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCTTGCACTCGGCCTGTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACTGGGTGTGGTGGCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGGAGCCTGTCTGGTTCTTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCACCCCTGACCCTCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTCTGCTGCTGTTTC  
CATGGCCAGCATTCTCCACCCTTAACCCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT  
CCCTGCCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAAA



## **FIGURE 9**

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVVPQASVPLLTDLAQWEPVLVPEAHFNASLTMYVCTPVPHPDPPMALSRTPTRQISSSDT  
DPPADGPSNPLCCCFHGFSTLNPVLRHLFPQEAFFAHPIYDLSQVWSVVSFAPSRGQALRRQA

### **Signal peptide:**

amino acids 1-47

### **N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

### **N-myristoylation site.**

amino acids 56-60

### **Amidation site.**

amino acids 70-74

## FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGAATGGGAGCCGCCCGCTGCTGCCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGACAGTCAACGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCTAAGC  
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAGACTG  
CGTGTTACGGAGATCGTGCTGGAGAACAACTATACGGCCTTCCAGAACGCCCGGCACGAGG  
GCTGGTTATGGCCTTCACGCGGCAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCACGC  
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGGAACCAAGCGCACAC  
GGCGGCCCCAGCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCTTGGGCCGCTCCG  
CACCCCTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCTGAGGGCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG  
CCCCAGGGGCGGCTGGCAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT  
GAGTGTCACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC  
CGCTGAAAGGTCAGCGACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCTCTAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCCAAACCTCTCTGGCTAGACTGTA  
GGAAGGGACTTTTGTTTGTTTGTTCAGGAAAAAGAAAGGGAGAGAGGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCAACCCCAACTCCAGGCC  
CGGAATAAAACCATTTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGLIGKPSGKSKDCVFTIIVLE  
NNYTAFQNAHREGWFMAFTRQGRPRQASRSRQNRQEAHFIKRLYQGQLPFPNHAQKQKQFEF  
VGSAPTRTRTKRTRRPQPLT

### **Signal peptide:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 9-13, 126-130

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

### **Casein kinase II phosphorylation site.**

amino acids 65-69

### **Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

### **N-myristoylation site.**

amino acids 69-75, 188-194

### **Amidation site.**

amino acids 58-62

### **HBGF/FGF family signature.**

amino acids 103-128



## **FIGURE 13**

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPÆELHNVQSVHTVYLYGNQLDEFFMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLLEELHLDNDSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMVRELNMNLLSCPTTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPITPDWDGRERVTPPISERIQLS IHFVND  
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNRYRAVEDTICSEATTHASYLNNGSNTASSHEQTTS HSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGCGCGCGCGGAGACAGAGGCGAGAGGCAAGAGCTGGGGCTCCGTCCTCGCTCCACGAGCG  
ATCCCAGGAGGAGCGCGCGCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCTGCC  
TCGCTTCCCAGGCGCGCGCGCTGCAGCCTTGCCTCTTGTCTGCGCTTGAATGCGAAAGATGCTGCGAGGCT  
GCTTTCTGCTGATCTCTGCGACAGCTCGTCTCTCTCTGCGAGGCCGAGGAGCGGTACGCTGGAGAGTCCATCT  
CTAGGGCGCAGACACGCTCGGACCCACCCGACAGCGCCCTTCTGGAGAGTTCTCTGTGAGAACAGCGCGGACAGC  
TGGTTTTCATCTTATGACGCTCTCGCAGTGTCAACCCCATGACTATGCAAAAGGTCAAGGAGTTCATCTGGGACA  
TCTTGCATCTTCTGACATTTGGTCTTGAATGTCAACCGAGTGGGCTGCTCCATATGGCAGCAGCTGTCAAGATG  
AGTTCTCTCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCTGCTGTCTCAAGGAGTSCGGCATCTGTCCAGCG  
GCACCATGACTGGGCTGGCCTCAAGTATGCCCTGAACATCGCATTTCTAGAGACGAGGGGGCGGCCCTTGA  
GGGAGAAATGTGCCACGGGTCTAATATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCGAGGTGGCTGCTA  
AGGCA CGGAGACCGGATCTCTTAATCTTGGCCATGAGTGGGAGCTCAGGACTCCGTGGCGAGGTGGCTGCTA  
GGAGTGAAGCCCATGAGGACATGTCTTCTTGTGGCCAAATTCAGCGAGATGAGACGCTGACCTCCGTTGTCC  
AGAAGAAGTTGTGCACGGCCCATGCTGTCAGCACCCCTGGAGCATAACTGTGCCCCTTCTGCATCAACATCCCTG  
GCTCATACGCTCTGAGGTCGCAACAGGCTACATTTCTCAACTCGGATCAGACGACTTGCAGAAATCCAGGATCTGT  
GTGCCATGGAGGACCACACTGTGAGCAGCTCTGTGTGAATGTGCCGGCTCTTCTCGTCTGCCAGTGTCTACAGT  
GCTACGCTCTGCTGAGGTGGGAAGAGTGTGTGGCTGTGGACTACTGTGCTCAGAAAACAGGATGTGAAC  
ATGAGTGTCTTAATGTGTGAGTGGCTCTTCTTGGCAGTGGCATGAAGGATTTCTCTTAACCCAGATGAAAAA  
CGTGACACAGGATCAACTACTGTGCACTGAACAAACCGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT  
ACTACTCGCGCTGCCACCGTGGCTACACTGTGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCTGCTGCCAGTGTCTCAGAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCGCGTGGATTAAGTCTGCTGAGTGAACCATGCTTGAATCTCTCT  
GTGTCAACATGACAGATCTTGTGCTCTGGGGGACCAAGTGTGAACATTCGTTGTGAAGCAGTGAAGATTCTGTTGT  
CAAAATTTGACTCTTGTGCTCTGGGGGACCAAGTGTGAACATTCGTTGTGAAGCAGTGAAGATTCTGTTGTGT  
GCCAGTCTTTGAAGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAAGAAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGAAGCTCATACAGCTGCGAGTGTCTGGAGGATTCGGCTCG  
CTGAGGATGGGAAACGCTGCGGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGGGAACACATTTGTGTTA  
ATAATGGGAATTCCTACATCTGCAATGCTCAGAGGATTTGTTCTAGCTGAGGACGGAAGCGGTGCAAGAAAT  
GCATGAAGGCCCAATTGACTTGGTCTTGTGATCGATGGATCCCAAGAGTCTTGGAGAGAGATTTTGGAGTCTG  
TGAAGCAATTTGTCACTGGAATTATAGATTCTTGAACATTTCCCCAAAGCCGCTGAGGCTGGGCTTTCAGCTCG  
ATTTCCACAGGTCACACAGAGTTTCACTCTGAGAACTTCACTCAGCCAAAGACATGAAAAAGCCGTTGGCCAG  
ACATGAAATACATGGGAAAGGCTCTATGACTGGCTGGCCCTGAAAAACATGTTTGAAGAGATTTTACCCAG  
GAGAAAGGGCCAGGCCCTTTCCACAGGGTGCCAGAGCAGCATTTGTGTTACCGCGGACGGCTCAGAGT  
ACGTTCTCCGAGTGGCCAGTAAAGCCAGGCCAATGGTATGATGCTGTTGGGTTAGGAAGACCATTTG  
AGGAGGAATCAAGAGATTTGCTCTGAGCCCAACAAAGCATCTCTCTATTCGCCAAGACTTCAGCACAATGG  
ATGAGATAAGTGAAGAACTCAAGAAAGGCATCTGTGAAGCTTGAAGACTCCGATGGAGAGCAGCTCTCAG  
CAGGGTAATCTGCCAAAACGGTCCAAAGCCCAACAGATCTGAGCAGTCAACATAAATTTCAAGACCTACTTT  
CTGTTGAACTTTTTCAGTGCACACAGATATCTGTTTGAAGAAAGCAATTTTACGGCTCTACACAAAAGCTTT  
CCATTTCAACAAACCTTCAGGAAGCCCTTGGAGAAACACAGATCAATGCAAAATGTGAAGCTTTATCTAGGA  
TCCAGAACCTTGCAGAACAGAAAGTGAAGAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAAATGGAAGCC  
TGGAAATCGCTGAGATACAGATGAAGATTAGAARTCGGCACACATTTGTGATTTGTGAAGTAAACATCAGTCTGA  
GAACGAGTGTGCCACAGAACCAAGACAGAAAGTATACACTACTTGTATAAATTTATCTAGGAAGAAATCTCT  
TCAGAAATCTAAGATGAATTTACAGGTGAGAATGAATAAGCTATGCAAGGATTTTGTATATCTCTGGAAC  
CACTTGTCTCTGCTCACTCGCTGCTAGTGTGCAATCTCATTTGACTATAGATAAGTTTGCACAGCTTTGAC  
TCTGTAGAACCTCGCCATAGGAATGCTGTTTTTTTGTACTGGACTTTACCTTGATATATGATATGGATGTAT  
CATAAAACTAGAGACATATGACTGTGGAACAAGTTGATTTTTTATACAAATTAATAATTCACCATCTCAG

## **FIGURE 15**

MEKMLAGCFLILGQIVLLPAEARESRGRSISRGRHARTHPTQTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNESLKTFFKRKSEVERAV  
KRMHRLSTGTMTGLAIQYALNIAFSEAEAGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSTVFQKKLCTAHMCSTLEHN  
CAHFICINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINICALNKPQC  
EHCECVNMEESYCRCHRGYTTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFII  
NEDLKTCSRVDYCLLSDHGCEYSVNMMDRSFACQCPEGHVLRSDGKTCAKLDSALGDHGCE  
HSCVSSSEDSFVCQCQFEGYILREDGKTCRRKDVCAIDHGCEHICVNSDDSYTCECLEGFRLA  
EDGKRCRRKDVCKSTHHGCEHICVNNNGSYICKSEGFVLAEDGRRCKKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKSGMTGLALKHMFERSFTQGEARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQEIASSEPTNKHLYAEDFSTMDIEISEKLKKGICEALEDSDGRQDS  
PAGELPKTVQQTSESEPTVINIQDLLSCSNFAVQHRYLEEDNLLRSTQKLSHSTKPSGSPLE  
EKKHDQCKCENLIMFQNLANEVVRKLTQRLEEMTQRMEALENRLRYR

### **Signal peptide:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 221-225

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

### **N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

### **Amidation site.**

amino acids 314-318, 560-564, 601-605

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTGACGGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCGAGCCTCG  
GCACCTGCAGGTCCTGCGTCCCAGCGGCTGGCGCCCCTGACTCCGTCCTCGGCCAGGGAGGGC  
**CATG**ATTTCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCAACCGGTGCGAG  
GCGGTGGAGGGAGGGGAAAGTGGTGCTCCAGCGTGGTACACCTTGACCGGGAGGTTGTCTTC  
ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAACTAGGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT  
GTGGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTCTTTGCACACGATTAGATGTCAATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCATGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTGGGTACCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC  
TCTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGACCTGCCCCTGGCCCAGAGCTCAGACACAATCTCCAAGAAATGGGACCTT  
TTCTCTGTCACTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCACACCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTAT**TGA**TGAC  
CCCACCACTCATTGGCTAAAGGATTGGGGTCTCTCCTTCCCTATAAGGGTCACTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGTACTACCAAGAGTGAGGGGCAGAGACTCCAGTCACTGAGTCTCCACGGC  
CCCCTTGATCTGTACCCACCCCTATCTAACACCCCTTGGCTCCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTGAGGCTGGCTTGGTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTC  
TTATTAATAACTAACATGAAATATGTGTTGTTTTTCATTGCAAAATTTAAATAAGATACATAA  
TGTTTTGTATGAAAAA



## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
SCSVNVQDKQKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCQSPRSKPAVQYQ  
WDRQLPSFQTFPAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA  
VVAGAVVGTLLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPPWKSSDTISKNGTL  
SSVTSARALRPPHGP RP GALTP T PSLSSQALPSPRLPTTDGAHPQPI SPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 245-267

### **N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

### **N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

[illegible]

GCCACCACCTGCGGCCACCGCCCAATGAACAGCCTCCGCTCCTAGTGGTTTTTTCCACTTTG  
TTGAATTTGTTCTATACATAAAATGCACCAAGACACCTTGCTCCCAAAATGCAAAATGTGA  
AATACGCAATGGAATTTGAAGCTGCTATTTGCCAACATGGGATTTTCAGGAATGTGTCACAA  
TTTGTGAAGATGATATAATGAATGTGGAAATTTAACTCAGTCCTGTGGCGAAAAATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTATTATGTGTGTACCTGGCTTCAGATCCAGCAGTAAACCA  
AGACAGGTTTTATCATAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATT  
TAGATAATGTCTGTATAGCTGCAAAATATTATAAAATCTTAAACAAAAATCAGATCCATAAAA  
GAACCTGTGGCTTTGCTACAAGAAGTCTATAGAANAATCTGTGACAGATCTTTTCAACCAAG  
TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATATAGTTTACAAGAACAAACA  
CTATCTCAGCGCAAGGACACCCCTTTCTAACAACCTCTTATGAAATTTGTAAAAACCGTGAAT  
AATTTTGTCAAAGGGATACATTTGTGATTTGGGACAGAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTTAAGGATATCCGACAGCTTCC  
AAAAAGCACAGAGTTTGATACAAATTTCAACGGATATAGCTCCAAAGTTTTCTTTTGTGAT  
TCATATAACATGAACATATCATCTCTCATTAATGAATATGATGGAGACTACATAAATATTATT  
TCCAAAGAGAAAAAGCTGCATATGATTCAAATGGCAATGTGTCAGTTGCATTTTTATATTATA  
AGAGTATTGGTCTCTTTGCTTTTCATCACTGACAACTCTTATTGAAACCTCAAATATTGAT  
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAAACC  
ACCCACATTTATGAACTTGAAAAAATAACATTTACATTAAAGTCATGAAAGGTCACAGATA  
GGTATAGGAGTCTATGTGCTATTTGGAATTTACTCAACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCTGTCGCGTGTAACTACCT  
GACACATTTGCAATTTTGTATGTCTCTGTGCTCTTCATTTGTTATTAAGCATTTATAATTTT  
TCACAAGGATCACTCAACTAGGAATAATTAATTTCTAGTAATTTGTCTTCCGATATGCATTTTT  
ACCTTCTGTTTCTTCAGTGAATTTCAAAGACACAGGACAACAATTTCAAAAAATCTTTGCTG  
TAGCCTAATTTCTTGCTGAACTTGTTTTCTTTGTTGGGATCAATACAAATACATAAGCTCT  
TCTGTTCAATCATTTGCCGGAGTGCTACACTACTTTCTTTTAGCTGCTTTTGCAATGGATGTGC  
ATTGAAGGCATACATCTTATCTCATTTGTGTGGGTGTCATACAAAGGATTTTTTGCA  
CAAGAATTTTTATATCTTTGGCATCTAAGCCAGCCGCTGGTATGTGGATTTTCCGCGAGC  
TAGGATACAGATATTATGGGCACAAACCAAGTATGTTGGCTTAGCACCGAAAAACACTTTATT  
TGGAGTTTATATAGGACAGCAGTGCCTTAATCATTTCTGTTAATCTCTGGCTTTTGGAGTCA  
CATATACAAAGTTTTTTCGTCAACTCGAGGTTGAAACAGGAGTTAGTTGCTTTGGTGAACA  
TAAGTCTGTGTGCAAGAGGAGCCCTCGCTCTCTGTTCTCTTCGCGACCACCTGGATCTTT  
GGGTTTCTCCATGTTGTGCGAGCATGAGTGGTTACAGCTTACCTCTTCAGCTGCAAGATGC  
TTTTCCAGGGGATGTTCAITTTTTTTTCTGTTGTTTATATAGAAAGTACAAGAGAAT  
ATTACAGATTTGTTCAAATAATGTCCTGTGTTTGTGATGTTAAGGTAACATAGAGAATG  
GTGGAATAATCAACTGCACAAAAATAAAATTTCAAAGCTGTGGATGACCAATGTATAAAAA  
TGACTCATCAAATTTATCCAATTATTAACTACTAGACAAAAAGTATTTAAATCAGTTTTTCT  
GTTTATGCTATAGGAACGTGTAGATAATAAGGTAAAAATATGTATCATATAGATATACATGT  
TTTTCTATGTGAATAGTTCTGTCAAAAATAGTATGCGATATTTGGAAGTAAATGGTTTT  
CTCAGGAGTGATATCACTGCACAAAGGAAAGATTTTTCTTTCTAACACGAGAAGTATATGAA  
TGTCTGTGAAGGAACCACTGGCTTGATATTCTGTGACTCGTGTGCTTTGAAACTAGTCC  
CTACACCTCGGTAAATGAGCTCCATACAGAAAGTGAACATAGAGAATGAAGGGCGACA  
ATATCAACACAGTGAAGGGAAGGATAGATGATTTTGTGAATGAACTGTTTTCTGTGAGC  
TAGCTGAGAAATTTGTGACATAAAATAAAGAATTTGAAGAAACACATTTTACCATTTTGTGAA  
TTGTTCTGAACTTTAAATGTCCACTAAAAACAATTAGACTTCTGTTTGTCTAAATCTGTTTCT  
TTTTCTAATTTCTTAAAAAATAAAGGTTTACCTCCACAAATTTGAAAAAATAAATAA  
AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

## **FIGURE 19**

MKRLPLLVPFSTLLNCSYQNTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIEENVNANCHLDNVCI  
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIIITYIEILAESSLLGYKNNTISAKDTL  
SNSLTLEFVKTVNNFVQRDTFVVDKLSVNHRRTHLTKLMHTVEQATLRISQSFOKTTEFDT  
NSTDIALKVFFFDSDYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFLYYKXSIGPLLS  
SSDNFLLKQPNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDTRYRSLCAF  
WNYSPDTMNGSWSSSEGCETYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSTIAGL  
LHYFFLAFAWMCIIEGIHLYLVVGVYINKGFLHKNFYIFGYLSPAVVVGFSALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLVHVASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEYYRLFKNV  
PCCFGCLR

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

### **N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

### **Glycosaminoglycan attachment site.**

amino acids 49-53

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

### **Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

### **Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

### **N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

000000000000

TGGAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT  
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATATGATAATCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAATAACATTTACATTAAAGTCATCGAAAGTCCAGATAGGTATA  
GGAGTCTATGTGGCATTTTGGAACTACTCACCTGATACCATGAATGCGAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTTGCAATTTTGATGTCCTCTGGTCTTCCATTGGTATTAAAGATTATAATATCTTACAA  
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTACCTTC  
TGGTCTTCAGTGAAATTCAAAGCACCAGGA

## FIGURE 21

GCTCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCTCTCTCTCCCGCAGATCCGAACGGCCTGGGCGGGGTCAACCCGGCTGGGA  
CAAGAAGCCGCGCCTGCTGCCCGGGCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG  
CCGCGCGCGCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCAGACCCCGCAGCGCATCCCGGTGCGCGCCCGAGCTCCCGACCCCATCGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTTGGCCGGCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGGACTGCGCGCGGGGG  
CAGAGCGCGCACAGTTTGTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG  
CGTGCA CAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCACT  
ACTCGGAGGAAGACTGTGCTTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTCTTCCACTCTCTCATTTCCCTGCCATGCTGCCCATGGTCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAACTGACATGTCTCTTCGCCCTCGGAGACCGACAGCATG  
GACCCATTGGGCTTGTACCCGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAACT  
GAGACCATGCCCGGGCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCTGTAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAGAGTTTTCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTTGGCCAGCTGCTGCTGGGCCCCCATCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
TCACTTCTTTGGAAAAATTCTTATGTCAAGCTGAAATTTCTAATTTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTTCAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCCACAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAAATTTCCC  
CTGAGGCCAGTTCTGTCAATGGATGCTGTCTGAGAATAACTTGCCTGCCGGTGTCACTGC  
TTCCATCTCCAGCCACCAGCCCTCTGCCCACTCACATGCCTCCCATGGATTGGGGCCT  
CCCAGGCCCCCACCCTTATGTCAACCTGCACCTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCAATAACTTGTGTGTGGGAAGCAGCGGGGAAGACCTAGAAC  
CCTTTCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTTCTTACATATTTTATGCCCCAAATATATTTATGTATGTAAGTGAGGTTTG  
TTTTGTATATTAAAAATGGAGTTTGTGTTTG

## **FIGURE 22**

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSILLEIKAVLRRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

### **Signal peptide:**

amino acids 1-22

### **Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

### **N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## FIGURE 23

CCCAGAAGTTC AAGGGCCCCGGCCTCCTGCGCTCCTGCGCGCGGGACCCCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCGGGGAAGATGGCGAGGAGAGCCGCCACCGCCTCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTGCCTCTGGGCTATCATAAGGCTATGGGTTTTCTGCCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA  
AGAAGACTGTTTTCTCCAGATTAGAGTGGAAGAACTGGGTGCGAGTGCTCTCTTTGTCTAC  
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCATCTG  
AGCAAGGCCAAAACTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACAAATGAATACAAAACTGGAAGT  
CTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC  
TGTGGATATCGCAGGTGCTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTCCAGAAGAGTAATTTCTTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCTGTAATCCAGCACTTTGGAAGG  
CCGCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC  
CATCTCTACTAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCATCTCAAAAAATAAAATAAAATAAATA  
AATAAATACTGGTTTTTACCTGTAGAATCTTACAATAAATATAGCTTGATATTCT

## **FIGURE 24**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQOTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCCEVPSSALSCTVVVELRCQDKEGNPAPEYTWFKDGI RLLENPRLGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNI SGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETS FQKSNSSSKATTMSENVQWLTPV I PALWKAAGGSRGQEF

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 130-144, 238-258

### **N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

### **Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

### **N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

### **Amidation site.**

amino acids 226-230



## FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAAACATGCTCCACAGCCCGGACCCCTGGCAT  
CATGCTGCTATTCTCTGCAAACTACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA  
ATGAATTACTCAATCTCTCTATGACCATTATACATATCCACCTTCAAAAAGTACATCAATA  
TTATATCATTAAGGAAATAGTAACCTTCTCTTCCAAATATGCATGCATGCTTTTGGACAATG  
CAATTGTGGCACTGGCACTTATTTCACTGAAGAAAACTTTGTGGTTCATATGGCATTATCA  
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACCTTACTAGCACTGCACTG  
TGGAATCCTTTAAGGGCCCATTAATTTCTGAAGAAGAAAGCTAAAGATGAAGGCATGCCACT  
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTTGTCACCGGTATGTACGTGTGAARTCAGGCCCTTGGTTTACACCCAGATCCATTTAT  
ATGGAAGCATCTCAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC  
AGCTAACACACAGATCTTCTCTACAGACTAACAAATATTGCAAAAATGAATACTCCCAAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAAACATTTATCTTCAGTCACCAAT  
ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACTTACTGA  
ACTGCCTGAAAAATGTCTGTCCGAACCTGAGCACTTACAAGAACCTCTATTAATCACAACCT  
TGCTTTCTACAATTTCACTGGAGCCTTATTGGCCTACATAATCTCTTCGACTTCACTCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCCAAATCTAGAGAT  
TCTGATGATTTGGGGAAAACTCAATTATCAGAATCAAAGACATGAACCTTTAAGCCTCTTATCA  
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTTGGTT  
GGACTGGAAAACTTAGAAAGCATCTCTTTTACGATAACAGGCCTTATTAAAGTACCCCATGT  
TGCTCTTCAAAAAGTTGTAATCTCAAATTTTGGATCTAAATAAAAATCCTATTAATAGAA  
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAAATAATGCCT  
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC  
TACTAACACCCCTAGATTGCTTACATTACCCCAATGCATTTTTCAGACTCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG  
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCTCCGTTG  
GATGAACATGAACAAAAACCAACTTCGATTTCATGGAGCCAGATTCACTGTTTTGCGTGGACC  
CACCTGAATTCGAAGGTGAGAATGTCGCAAGTGCAATTTAGGGACATGATGGAAATTTGT  
CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT  
TTCCTTTCACTGTAGAGCTACTGCAGAACCAAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAAACCTTGGCTAATACCTTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA  
GATATAAATGGGCTAACTCCCAAGAAGGGGTTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGTACAACATG  
GCTCTTTGAATATTAATAAAGAGATAATCAGGCCAATTCAGTTTTGGTGTCTGGAAAGCA  
AGTTCTAAATTTCTCAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAAATTTCA  
TGCTGCGCAAAGTGCTCGAATACCATTGATGTCGAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTTGATTTGATATTCCACCATTCTATCAGAAAAACAGAAAAAAA  
TGTGTAATGTCAACCAAGAGTTTGCACCCCTGATCAAAAAGAGTATGAAAAAATAATAC  
ACAACACTTATGGCTGTCTTGGAGGCCCTCTGGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTTACTTACAG  
AAACCAACCTTTGCATTAGGTGAGCTTTATCTCTCTGATAAATCTCTGGGAAGCAGGAAA  
AGAAAAAGTACATCACTGAAAGTAAAAGCACTGTTATAGGTTTACCAACAAATATGTCTT  
AAAAACCAACGAAGAACTACTCCAAAAATGAAC

## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPEARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSVLVIAGINLITEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVYNLKFDDLKNPINRIRRGDFSNMLHLKELGINNPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHNAFFRLPKLESMLNLSNALSALYHGHTIESLPNLKEISIHSPNIRC  
DCVIRWMNMNKTNIIRFMEPDSLFCVDPPPEFQGNVRQVHFRDMMEICLPLIAPESFPSPNLNV  
EAGSYVSFHCRTAEPPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNLIKIRDIQANSVLVSWKASSKILKSSSVKWTAFV  
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLGIIGVICLISCLSPMNCDGGHSYVRNYLQKPTFALGELYPPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

### **Signal sequence:**

amino acids 1-22

### **Transmembrane domain:**

amino acids 633-650

### **N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

### **Tyrosine kinase phosphorylation site.**

amino acids 570-579

### **N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

### **Cell attachment sequence.**

amino acids 277-280

00000000000000000000000000000000

CCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC  
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCAGCAGATGAATCT  
GGTAGACCTGTGGTTAACCCTTCCTCTCCATGTGTCTCCTCTACAAAGTTTTGTCTCTTA  
TGATACTGTGCTTTCACTTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG  
GGTTTTAAATGTCACTCTGTAGCAATGCAAAATCTCAAGGAAATACCTAGAGATCTTCCTCTCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTTAGTTTTCTCATGAGCAT  
GCCTTCAAAGGAGTAGCTGAACCTCTGTGAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCACAACCCCTGGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCCAC  
AACGTGATCTGTAAAAAGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGTCTGC  
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG  
GATGCCCGGAGACACCTCGAATTACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGCTGTCCAAACTGACTGTCTATTGAGAAAGAAAGAAA  
GTAGTTTGCATTGCACTAGAAAATAAGTGGTTTTACTTCTCCCATCCATTGTAACATTTGAA  
ACTTTGTATTTCAGTTTTTTTTTGAATTATGCCACTGTGAACTTTTAAACAAACACTACAACA  
TAATAATTATTGAGTTTAGGTATCCACCCTTAAATGTACCCCGATGGTATATTTCTTGAGT  
AAGCTACTACTCTGAACACTTAGTTAGATCTCATCTCACTATTTAATGAAATTTATTTTTTT  
AATTATAAAGCAAATAAAGCTTAACTTTGAACCATGGGAAAAAATAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLLQS FVLMILCFHSASMCPKGCLC SSSGGLNVTC SNANLKEIPRDL  
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNR  
IQSVHKNAFNNLKARARIANNPWCHDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL  
NAANDADLCNLPKKT TDYAMLVTMFGWFTMVISYVVVYVRQNQEDARRHLEYLKS LPSRQKK  
ADEPDDISTVV

### **Signal sequence:**

amino acids 1-33

### **Transmembrane domain:**

amino acids 205-220

### **N-glycosylation site.**

amino acids 47-51, 94-98

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

### **Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

### **N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## FIGURE 29

ACCGAGCCGAGCGGACCGGAAGGCGCGCCCGAGATGCAAGGATGCTGGCGGGG  
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCATCTCTGCTGGTGTCT  
GGGCTCAGTGCTGTCAAGCTCGGCCACGGGCTGCCGCCCGCTGCGAGTGCTCGGCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG  
ACGGCCTCTGTGGACCTAGGCAAGAACCGCATCAAACGCCTCAACAGGACGAGTTCCGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCTGTAGCGCCGTGGAGCCCGGCG  
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAAACAAGAT  
CGTTATCTCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCTCACCGCGCTTCAGCGGCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTTCCCCACCTGCACGGCT  
CATCGTCTTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCTTCAAGAGGC  
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC  
TGCCTCTACGGCTCAACCTGACGTCCCTGTCCATCACACTGCAATCTGACCGCTGTGCC  
CTACTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCTCAACCTCTCTTACAACCCCATCA  
GCACCAATTGAGGCTCCATGTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC  
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCTCAACTACCTGCGCGTGTCAA  
TGTCTCTGGCAACCACTGACCACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG  
AGACACTCATCTGGACTCCAACCCGCTGGCTGCGACTGTCCGCTCCTGTGGGTGTCTCCGG  
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCCGAGTTTGTCCA  
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACTGCCGCCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGGCCACACGGTGCAGTTT  
GTGTGCCGGGCCGATGGCGACCCGCGCCCGCCATCTCTGGCTCTACCCCCGAAAGCACT  
GGTCTCAGCCAGAGCAATGGGCGGCTCAGAGTCTTCCCTGATGGCAGCTGGAGGTGCGCT  
ACGCCAGGTACAGGACAACGGCAGCTACTGTGCATGCGGCCAACGCGGGCGGCAACGAC  
TCCATGCCCGCCACCTGCGATGTGCGCAGCTACTGCCCGACTGGCCCATCAGCCCAACA  
GACCTTCGCTTTCATCTCCAACAGCCGGGCGAGGAGAGGCCAACAGCACCCGCGCCACTG  
TGCCTTTCCCTTTCGACATCAAGACCTCATCATCGCCACCAACCATGGGCTTCTATCTTTTC  
CTGGGCTCGTCTCTTCTGCTTGGTGTGCTGCTTTCTCTGGAGCCGGGCAAGGGCAACAC  
AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGAGGCATCAGCTCCGCCG  
ACGCGCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGCGGGGGCAGGACCCCCG  
GGCGCCGGGCGAGGGAAGGGGCTGGTCGCCACCTGCTACTCTCCAGTCTTCCCACTC  
CTCCCTACCTTCTACACAGTTCTCTTTCTCCCTCCCGCTCCGTCCCTGTGCCCCCG  
CCAGCCCTCACCACCTGCCCTCTTCTACACGAGACCTCAGAAGCCAGACCTGGGGACCCCA  
CCTACACAGGGGCAATTGACAGACTGGAGTTGAAAGCCGACGAAACGACACGCGGACAGTCA  
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTTCAATAATTATGAGTTT  
TATGAAAACCTTGAAATAATAAAAAAGAAAAAACTAAAAA

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFFNNLFNRLTL  
GLRSNRLKLIPLGVFTGLSNLTQKDISENKIVILLDYMFPQDLYNLKSLEVGDNLDVYISHRA  
FSGLSNLEQLTLEKCNLTSIPTALSHLHGLIVLRLRHLNINAIIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSIHCNLTAVPYLA VRHLVYLRFLNLSYNPISTIEGSMLHEL  
LRLQETQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSGVGNLETLILDSNPLA  
CDCRLLWVFRRRWRLNFNROQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVPDGTLEVRYAQVDNGTYL  
CTAANAGGNDMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPPFFDIKTLI  
IATTMGFISFLGVVLFCLVLLFLWSRGKNTKHNIEIYVPRKSDAGISSADAPRKFNMKMI

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 556-578

### **N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

### **Tyrosine kinase phosphorylation site.**

amino acids 590-598

### **N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCATCCCCAGCCCCGGGGATTTCAGGCTCGCCAGCGCCAGCC  
AGGGAGCCGCGCGGAAGCGCGATGGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC  
TGTTTCGCTGCTGCTGGGCGCCCGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGCCCGTGGTCTCAAGTGCCAAGTGAAAGATCA  
CGAGGACTCATCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTTCAGCTGGTTACCTCTACGCCCCAGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
GCGAAGTGCCTGCTCGTCACTGTGCTAGGAATTCACAGAAGCCATCATCACTGGTT  
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTGCTAGTCTTCTGGGAGCAAG  
CCTGCAGCCCGGCTCACCTGGAGAAAGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAAACTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTTATACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCTCTGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCAGGAGAGT  
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCTT  
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTCTGCTG  
CTCATCATGCTCATCTTCCTTGGCCACTACTTGATCCGGCACAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACAGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGACGACAAGAAGGAATATTTATCTAGAGGCGCCTGCCACTTTCCTGC  
GCCCCCAGGGGCCCTGTTGGGACTGCTGGGGCGTCACCAACCCGACTTGTACAGAGCAA  
CCGAGGGCCGCCCTCCCGCTTGCTCCCCAGCCACCCACCCCTGTACAGAATGTCTGC  
TTTGGGTGCGGTTTTGTACTCGTTTTGGAATGGGGAGGAGGGCGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTTCGTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA  
AACAAAAACA

## **FIGURE 32**

MGAPAAASLLLLLLFACCWAPGGANLSQDDSQPWTSDET VVAGGT VV LK CQVKDHEDSSSLQW  
SNPAQQOTLYFGEKRALRDNRIQLVTSTPHEL S I S I S NVALADEGEYTC S IFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRI QEDPNGK  
TFTVSSSVTFQVTRREDDGASIVCSVNHESLKGADRSTSQR IEVLYTPTAMIRPDPPHPREGQ  
KLL LHCEGRGNPVPQQYLWEKEG SV PPLKMTQESALIFPFLNKSDSGTYGCTATS NMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLI MLI FLGHYLI R HKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 331-352

### **N-glycosylation site.**

amino acids 25-29, 290-294

### **Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

### **N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



# FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCAACCCCAACCCCTTTTCTTCTCCTTTCTCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTTGAATGTGTCTGTGGCGAGCAGGATGGTCTGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGTCTTTGGATTTCTGTT  
GCTGGAGACGCTCTCTTTGTTTTCGCCGCTGGAACCGTTACAGGGGACGTTTGCAAGAGAGA  
TCTGTTCTGTCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTTCACA  
AGTCTGCAGCGTTTCACTGCCCGACTTCCCAGTTTTACCATTATTTTCTGCATGGCAATTC  
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG  
AAACAATGGCTTG CATGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTGCCCATCACCCACTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGTAGAGGATAACCCCT  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAAACATTCCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACAGACTGCAGGGTAAAGACCTCAATGAAAC  
CAGCGAACGAGCTTTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGCGCCCCCTG  
CCCAAGAAGAGACCTTTGCTCTCGGACCCCTGCCAACTCCTTTCAAGACAATGGGCAAGAG  
GATCATGCCACACAGGGTCTGCTCCAACCGGAGGTACAAGATCCCAGGCAACTGGCAGAT  
CAAAATCAGACCCACGAGCGATAGCGAGGGTAGCTCCAGGAACAACCCCTAGCTTAACA  
GTTTACCTCGCCTGGGGGCTGCAGCTGCGACCAATCCAGGGTCTGGGTTTAAAGATGAAC  
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA  
GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAAATCGCACTTTTGTGGATTACAAGA  
ACCTCATCTGTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACCAACACTTTCAAG  
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTAACCTGGACACGCTGTGCCGGGA  
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCCGGGCACTTTCAATGCCATGCCAAACTGAGGATCCTCATTTCTAACAACAACCTG  
CTGAGGTCCTGCTGGAGGTGTTGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCAACA  
CAATTACTTATGTACTCTCCCGTGGCAGGGGTGCTGGACCACTTAACCTCCATCATCCAGA  
TAGACCTCCACGGAACCCCTGGGAGTGTCTCTGCACAATTTGTGCTTTCAAGCAGTGGGCA  
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGTGAACCTTCTT  
TAGAAAGGATTTATGCTCTCTCCAATGACGAGATCTGCCCTCAGCTGTAGCTAGGATCT  
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGACGCACTCC  
AACTCCTACCTAGACACCAAGCAGGGTGTCCATCTCGGTTTGGTCCCGGGAGCTGCTGTGGT  
GTTTGTACCTCCGCCTTCAACCGTGGTGGGATGCTCGTGTATTACCTGGAGAACCGAAGG  
GGTCCAAGAGACGAGATGCCAACTCTCCGCGTCCGAGATTAATTCCTACAGACAGTCTGT  
GACTCTTCTACTGGGCACAATGGGCCCTTACAACGAGATGGGGCCCAAGAGTGTATGACTG  
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCAATAGGGAGGGCAGGAGGGAAGGCG  
ATACATCCTTCCCACCGCAGGCACCCCGGGGCTGGAGGGGCGGTGTACCCAATCCC CGC  
CCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTCGCACAAACCGAAAGGGCCT  
GACCCCTTACTTACTGCTTCCCTTGAACAACAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA  
GCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAAGCCGACGACGACCTGTCTGGAAG  
AACTGACAGTGCCTTCCGCTCGGCCCGGGGCTGTGGGCTGGATGCCCGGCTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCTGTGGCTACGACGGGATGGGCAGTTGACAGAGGCATGAATGTAT  
TGTAATAAGTAACCTTGAATCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSSQFYH  
LFLHGNSLTRLFNEFANFYNAVSLHMENNGLEIIVPGAFLGLQLVKRLHINNKKIKSFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAQFDLNLKLEVLILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPEYBEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPKLN RVDS SLPAPPAQEETFAPGPLPTPFKTINGQEDHATPGSAPNGGTK  
IPGNWQIKIRPTAAIATGSSRNKPLANS LCPGGCSCDHI PGSG LKMNCNNRVSS LADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLDDLRLWLYMDSNY  
LDTLSREKFAGLQNL EYLNVEYNAIQLILPGTFNAMPKLRILILN NNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSC TIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLLVFVTS AFTVVGMLVFILRNKRKSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 618-638

### **N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

### **Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

### **N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTCGACCCAGAAATAACTCAGGGC  
TGCAACCGGCCCTGGCAGCGCTCCGCACACATTTCTGTGCGGCCCTAAGGGAAACTGTTGGC  
CGCTGGGCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTTCGTGCGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCTCGAGCGGGAAGATCCAAGTTGGGAGCAGCTCTGCGTGGCGGGCCTCAG  
AGAATGAGGCCGGCGTTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCGGGCCGGCGG  
CGGCGAACACCCCACTGCCGACCGGTGCTGGCTGCTCGGCCCTCGGGGGCCTGCTACAGCCTGC  
ACCAACGTACCATGAAGCGGCAGGCGGCCGAGGAGCCTGCATCTCGAGAGTTGGGCGCTC  
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG  
GCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT  
GCACCTTGAGAACGAGCCTTTGCGGGGTTCTCCTGGCTGTCTCCGACCCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCAACGGGTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGG  
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTGTGTCCCTGCCCC  
GGGAGGTACCTCGCTGCTGCCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG  
CTTTGCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA  
GTGGGGAAGGACAGCGACCTTTGGGGGACCGGGGTGCCACACAGGCGCCCGCGGCCACT  
GCAACCGACCCCGTGCGCGAGAGAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC  
ACCACTTGTCCCTGAACAAGACAATTACAGTAACATCTATTCCTGAGATTCTCGATGGGGAT  
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTCCAAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT  
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT  
TGACCATGACAGTACTGGGGCTTGCAAGCTCTGCTTTACGAAAGCCCTCTTCCAGCCA  
AGGAAGGAGTCTATGGGCCCGCGGGCCTGGAGAGTGATCCTGAGCCGCTGCTTTGGGCTC  
CAGTTCTGCACATTGCACAAACATGGGGTGAAAGTCGGGAGCTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCCTGTGCGGGAGTCCCTCCTGGCTCTAGTGATGATAGGGAAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTTTCATCTTTGATGAAACGGGGAACCAAGAGGAACCTTAC  
TTGTGTAACGTGACAAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACATCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCCTTAGGA  
TGGTGATCTAGGGGACCGGGTAGTGCTGGGGAGAGATATTTCTTATGTTTATTCCGAGAA  
TTTGAGAGAAGTATTTGAACCTTTTCAAGACATTGGAACAAATAGAACACAATATAATTTACA  
TTAAAAATAATTTCTACCAAAATGGAAGGAAATGTTTCTATGTTGTTGAGGCTAGGAGTAT  
ATTGGTTCGAAATCCAGGGAAAAAATAAAAAATAAAAAATAAGGATTGTTGAT

## **FIGURE 36**

MRPAPALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA  
ASNL SYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACATGFE LGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMTVLGLVKLCFHES PSSQPR  
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAGALLAESPLGSSDA

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 399-418

### **N-glycosylation site.**

amino acids 189-193, 381-385

### **Glycosaminoglycan attachment site.**

amino acids 289-293

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

### **Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

### **N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGCGTGGGATTAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAAACTAAG  
CGTCGAGTCAGACGGGACCATAATCGCCTTTAAAGTGCCTCCGCCCTGCCGCCGCGGTATC  
CCCCGGCTACCTGGGCGCCCCCGCGCGGTGCGCGCTGAGAGGGAGCGCGCGGGCAGCCGA  
GCGCCGCTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA  
GGGCGCTGTGTGCCGGCGCGCGCGCGCGTGGGGTGCAAAACCCGAGCGTCTACGCTGCCATGA  
GGGCGCGCAACGCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTTCACATGTGGTGGCATTTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTTCCTGGAGTGTACCTCCAAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCGCGAAGGAAAAGTAGTCGTTCTCAATTTCGATTTCATAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG  
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC  
CCCCAATGGCCAGACCGGATTACCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTCAGT  
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA  
AAACTGCCTACAACACAGCCTGTCAACACCACATTTCCGTAAACCCAGGGTTTAAA  
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTACAGCAGGCGGG  
CAAGAACATGAGTGCCAGGCTGACTGTGCTGTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC  
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAACACAGC  
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG  
TTAAAGTGAAGTGTGCCATTTAAGCTGTATTCTGCCATTGCCCTTTGAAAGATCTATGTTT  
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT  
TGCTGTGTGCAGAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA  
AGCTAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTTATTTATACATCTCTGTAAAGGAT  
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTATAGT  
GTTATTGTGTTTCACTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGGTCTTCTA  
AATCAATGCTTAATAAAATATTTTAAAGGAAAAA

CGGACGCGTGGGATTAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAAACTAAG

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFCTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLES DNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEFNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTLGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

### **Signal sequence:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 355-359

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

### **Tyrosine kinase phosphorylation site.**

amino acids 199-208

### **N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

### **Cell attachment sequence.**

amino acids 149-152

## FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGGGCTGGGGCGGTGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCTCAACCTCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCTACCTG  
CCGGGGACTGGTTGACAGCTTTAAACAAGGGCTGGAGAGAACCATCCGGGACAACCTTTGGAG  
GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCTG  
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCCGCTGTCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGAGGCACCTTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGTGAGGCCCTGTGGCC  
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT  
TTTGGCCCTGTGCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTAAGAAGTGAGCCCTGGCTATCA  
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCGGGAGAGA  
ACAAGCAGTGTGAAAAACCGAGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTGTCAGCAGATGTTCTTTGGCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTGAGAGCGAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTGGAGTGGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTTCACTGGCGGGGACTGGCAGGCTTCAATGTGTGA  
ATTTCAAAGTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGTAGGATTAGGTG  
GTCTTCAAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGATGCTGCCAGTTCCTGT  
TCTGTGTTCAACACATCCCCACACCCATTGCCACTTATTTATTCATCTCAGGAAATAAGA  
AAGGTCTTGGAAGTTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEEENLSKYKDS ETRLVEVLEGVCSKSDFECHRLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQAG  
YGGEACGQCGLGYFEARNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCV DIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGFGRCKKCSFGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVLVQQMFPG  
IIICALATLAAKGDVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

### **Signal sequence:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 372-395

### **N-glycosylation site.**

amino acids 79-83, 205-209

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

### **Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

### **N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

### **EGF-like domain cysteine pattern signature.**

amino acids 181-193



## FIGURE 41

TGAGACCCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCCTTGTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACCTCTGGGTGTGCCCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGTGCGGCAGCTGCAGCTCAAAGAGGT  
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGGCCAGT  
ACGTGGCCCTGTCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTACGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGTGGTGTTCGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGACGGCCGTGTGCGGCTCTTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGTGTCCCCGCGCAGCGCCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGTGGAAGGCCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCCGTGACAGG  
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTTGCTCGCAGGGGGC  
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCTGAAGCACCATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTCAAGTGGC  
CGTTTCTGGGGCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCCGAGTGGTCAGCCTGCCCAACATGAGGGTGACAGAA  
GTGACAGCTGTGCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGGCAGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG  
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA  
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATCTACTGCACTATATTCTAAGCACTTACAT  
GTGGAGATACCTGTAACCTGAGGGCAGAAAGCCCANCTGTGTCATTGTTTACTTGTCTGTGCAC  
TGGATCTGGGCTAAAGTCTCTCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAAGACTTGTAAAACATGAATAAAACATTTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFSQSFFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEF  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTAVNF  
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRVFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTROPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSASDGALVPRRLQP

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 158-162

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

### **N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

### **Amidation site.**

amino acids 74-78

### **TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGGACAAA  
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGGAGTGTTACAGTGCACCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT  
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGGAAGTTTGACCA  
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGGCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCTCTGCCACCATTGGGAACCGGG  
CAGTGTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGAATGCCTACGAATCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCTCT  
GAATCCCAACAACAGGAGAGCTGGTCTTTGATCCCCGTGCAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCCATGGGAAGCT  
GTGGAGCGGAATGTGGGGTGCATCGTGGCAGCCGTCTTTGTAACCCTGATTCTCTGGGAAT  
CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCCAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTGGCCTTACT  
CAGGTGTACCGGACTCTGGCCCCGTGATGTCTGTAGTTTCACAGGATGCCTATTTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTGAGCTATGTGCCCC  
ATCCTCCTTCATGCCCTCCCTCCCTTCTCTACCACTGCTGAGTGGCCTGGAACTTGTTTAAA  
GTGTTTATTCCCCATTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAAATGGCGGGGGTGCAGGAATCTGCACTCAACTGCCCACTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG  
TGATGACACTGGGGTCTTCCATCTCTGGGGCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
CCACTGGGATCCCTCTGCCCTGTCCCTCCTGAATACAAGCTGACTGACATTGACTGTGCTGT  
GGAAAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAGAGAACTGAAGCAAAAG  
GATTTTAAACCCTGCTCTAAAGAAAAAGAAAACTGGAGGCTGGGCGCAGTGGCTCACGCCTG  
TAATCCCAAGAGCTGAGGCAGGCGGATCACCTGAGGTGCGGAGTTCGGGATCAGCCTGACCA  
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCGTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYSGFSSPRVEW  
KFDQGDTRRLVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYTCMVSEEGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPTSNAVRMEAVERNVGVIVA AVLVTLLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 238-255

### **N-glycosylation site.**

amino acids 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

### **Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

### **N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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CAGCGCGTGGCCGGCGCCCGCTGTGGGGACAGCATGACGCGCGGTTGGATGCGCAGGTTGGA  
GCGTGGCGAAACAGGGGCTCTGGGCCCTGGCGCTGCTGCTGCTCGGCCCTCGGACTAGGCCT  
GGAGGCCCGCGCAGACCCGCTTTCCACCCGACCTCTGCCAGGCCGCGAGGCCCCAGCTCAG  
GCTCGTGCCCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCCCTCACCTG  
CGCTGCGACAGGGACTTTGACTGCAGCGATGGCAGCGATGAGGAGGAGTGAGGATTAGGCC  
ATGTATCCACAGAAAGGGCAATGCCACCGCCCCCTGGCCCTCCCTGCCCTGCACCGGCGTCA  
GTGACTGCTCTGGGGGAAC TGACAAGAAACTGCGCAACTGCAGCCGCTGGCCCTGCCTAGCA  
GGCGAGCTCCGTTGTCACGCTGAGCAGTACTGTCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCGAGACTGTCCCGACTCTCAGCGACGAGCTCGGCTGTGGAAAGTAACGATCTCTCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCTTGGAGAGTGTCCCTCTGTGCGGAATGCCAATCTC  
ACAACCATGGGGCCCCCTGTGACCTTGGAGAGTGTCCCTCTGTGCGGAATGCCAATCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCGAGCTGCTGCGGTGC  
TCAGTGCAAGCCTGGTCAACGCCACCCTCCTCCTTTGTCTGGCTCCGAGCCAGGAGCGC  
CTCCGCCCACTGGGGTTACTGGTGCCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC  
CTCGCTGCCCTTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGCGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGGAGTAGGATGGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCCAGGACCTCCCAAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL  
RNC SRLACLAGE LRCTLSDDCIPLTWRC DGHPCPDSSDELGCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSIP

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 230-246

### **N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

### **Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

### **N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

### **Leucine zipper pattern.**

amino acids 17-39

## FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGGCACAGATGCGG  
 GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAACTGCATGCATGAGACCCACAGA  
 CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGATCATGGAATGAACCCGAGCAATG  
 GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
 GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT  
 CGATGACCTTCAAGTGTGTCTGACCCCGGCATTCCCAGAAATGGCTTCAGGACCCCCAGCG  
 GAGGGGTTTCTTTGAAGGCTCTGTAGCCCGATTCTCACTGCCAAGACGGATTCAAGCTGAAG  
 GCGCTACAAAGAGACTGTGTTTGAAGCATTCTTAATGGAACCTTAGGCTGGATCCCAAGTGA  
 TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTGATA  
 ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGATGAAGGATTCAAGATCCGG  
 TACCCCGACCTACACAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
 CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC  
 TCCAGACCTCCTTCCCGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTAAACTT  
 GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCAGCCACCCCGGTG  
 CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCGTCT  
 GCCACCCGCGCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTACTGCGATCCT  
 GGTACAGCCTCACACGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC  
 TTATCAAGTCTACTGCATCAAATCAGAGCAACGTGGCCAGACCCATGAGACCTCCTGA  
 CCACGTGGAAGATTGTGGCGTTACCGCAACCAGTGTGCTGCTGGTGTGCTGCTGCTGCTCATC  
 CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCTCCCCGGAG  
 TTCAGCAGTGACCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTATG  
 ACGAAGCTGTGAGTGGCGGCTTGAGTGCCCTTAGGCCCGGGTACATGGCCTCTGTGGCCAG  
 GGCTGCCCTTACCCGTGGACGACAGAGCCCCCAGCATACCCGGCTCAGGGGACACGGA  
 CACAGGCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAA  
 GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCTGCTTCGGACAAACCTGACATA  
 ATTGCCAGCAGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCCACTGGGT  
 GTTGTTCCTAAGAACTGATTGATTAAAAAATTTCCAAAGTGTCTGAGTGTCTCTTCAA  
 ATACATGTTGATCTGTGGAGTTGATTCCTTTCTCTCTGTTTTAGACAAATGTAAACAA  
 AGCTCTGATCCTTAAATGTCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
 CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAGNAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQPQSPQRL LAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETILLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQCPLPVDQSPPAYPGSGD TDTGPGSETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVFLRN

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 325-344

### **N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

### **Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

### **N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405



## FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTTCGGTGGCCTAGAGA  
TGCTGCTGCCGCGGTTGCAGTTGTTCGCGCACGCCTCTGCCCGCCAGCCCGCTCCACGCGCGT  
AGCGCCCGAGTGTTCGGGGGGCGCACCCGAGTCGGGGCCATGAGGCCGGGAACCGCGCTACAGG  
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC  
TCGGATTGTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCCTTGTTA  
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA  
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT  
CACAAATTTAGGAACTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCAGTGGAATGATGA  
CCGGTGAACATGAAGAACAAATTCATTTGCAAATATTCTGATGAGAAACCGAGGTTCCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG  
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT  
CCTAATCCCCAGCATTCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAAGCAACACACCATC  
TGGCCCTCTCCTCACCAGGGAACAGCCCGGACCTAGAGGTCTACAATGTGATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGCGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT  
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAAATGGCTGTGAACCCATCA  
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTTATGA  
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAAATGAAATATATG  
GTTATTAGGACATATAAAAAACTGAACTGACAACAAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCTCTGT  
GGATGAGCATGTGGTCCCCAGACCTCCTGTTGGACCCCCACGTTTTCGGCTGTATCCTTTAT  
CCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG  
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAAACCACTCTGTTTTCTTGTCTTATACAG  
CAGCACATATTATCATAACAGACAGAAAATCCAGAATCTTTTCAAAGCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAA

CCGCGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTTCGGTGGCCTAGAGA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGD F W I G L R R R E E K Q S N S T A C Q D L  
YAWTDGSISQFRN W Y V D E P S C G S E V C V V M Y H Q P S A P A G I G G P Y M F Q W N D D R C N M K N N F I C K Y  
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAAALNLAYILIPSIPLLLLLLV  
VTTVVCVWVICRKRKREQPD PSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETR PDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 117-121, 312-316

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

### **Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

### **N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGCGGCCGCAGAAAGACTTGT  
GTTTGCCCTCCTGCAGCCTCAACCCGAGGGCAGCGAGGGCCTACCACCATGATCAC'TGGTGT  
GTTTACGATGCGCTTGTGGACCCAGTGGGCGTCTGACCTCGCTGGCGTACTGCTCAGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCCGAGC  
CTGCTGAAGTTGAAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAAACCCAGCTATTAGAGGTCCCACCCCAAACCTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCCCTGAAGGGGGCATGTTTGTCTGGGAGTGTGACCAAGGTGGGCAT  
GCAGCAAATGTTTGCCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCTTTTC  
TTTACCAAACCTTCAACCCACAGGAGGTCTTTATTGCTTCCACTAACATTTTTTCGGAATCTG  
GAGTCCACCCGTTGTTTGTCTGGCTGGGCTTTTCCAGTGTGAGAAAGAGGACCATCATCAT  
CCACACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAGAGGCCGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGATACATACTGCCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCCTTTGCT  
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTGGCCCTGATGGGCTCTGCCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGAAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT  
TTAAATAAAGTGCCTTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFCQCKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFPLHILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMVEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTTAACATACTGTCAGCTAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTTTCAGCTCATCACCTTTCACCTGCCTTGGTCAATGGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGTCACCAGACCTGGATTCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCCTGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA  
GTCCCAGAGGGTGTACGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA  
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAGGTGG  
TGTGCCGCGAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAAACCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA  
GGATTGCCCTTCTGGGCCCTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCTG  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA  
CCAGGTGATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA  
AATGCTATGGCCCTGGGGTGGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTTCAGACTGCACCCACCAGGAAGA  
TGTGGCTGTCTATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACAGAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA  
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTTCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA  
CACCATTGTGCTGTTTCTCTGAAGAACTCTGACAAATAAGATTTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTTTAAGGATAAAATTTCTGAATTTGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACTTTATTTACAATAATAAGATAGCAC  
TATGTGTTCAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPEAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSFPVPEGVRLADGPGHCKGRVEVKHQNQWYTVTCQTGWSLRRAKVVCRLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKGWVGSVCDNNGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

### **Signal sequence:**

amino acids 1-15

### **Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

### **N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

### **Amidation site.**

amino acids 196-200

### **Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

ACTGCACCTCGGTTCTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTCCGGCTGCCTGGG  
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCATACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACC GCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGG  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTTGGCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTTGTGCCATCAGCAGATCCAGGGCAAG  
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA  
CTGCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTCTGTAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA  
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAAGACGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGTGTGAGACTTTAATGGAGATTGTCTCACAAGTGGG  
AAAGACTGAGAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA  
AGCTTCTTCCAGGGTGAGGGGAACACTTAAGAAATAAATATGGAGCTGGGGTTTAAACAT  
AAAAAAGTAAATAAACATCTCAACAGTAAAAAAGGCGCGGCGCATCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTGTTTATTGAGCTTTATAATGGTTAT

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVTGATSGLGKECAKVFYAAGA  
KLVLCGRNGGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDDTVDDVKRVMETNYFGPVALTALLPSMIKRRQGHIVAIISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRTLAPGLFFSILMASRARKERKSKNS

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 104-120, 278-292

### **N-glycosylation site.**

amino acids 228-232

### **Glycosaminoglycan attachment site.**

amino acids 47-51

### **Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

### **Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

### **N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

### **Amidation site.**

amino acids 265-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17



## FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCTCTAAAAGCAGTTTAGAGTGGTAAAAAA  
AAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC  
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCCTCGTGAAGCTTTTTATTCCTAA  
GAGGAGAAAATCAGTCACCGCGCAAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCCTGGGATATAAATAAG  
CATGGA CTGGAGGAAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTCATACCTTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAAGAAGGTGAAGGCAGAAATG  
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGTCTACA  
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCAATTCTTGGACTACAAA  
GGCATTCTCTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG  
CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGTCTGTGTTGGA  
TTTCATAAACTTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG  
TCTGTGTCTTAATTTCTGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT  
CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATAGCACCCTAGTTTTCTGAAAAGTATTACCAGGTTTAGGTTGATGTCATCTA  
ATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTCTAATATCCCCATTTCTTCAATA  
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCCTGTGTTCTTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTTATTAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
AATTTGTACCATAACCGTTTATTTAACATATATTTTATTTTGTATTGCACTTAAATTTTGT  
ATAATTTGTGTTTCTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA  
TGAAGGACTATATCTAGTGGTATTTTCAATGAATATCATGAACCTCTCAATGGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
AA  
AA

CGCGTCCGCTGGTGTAGATCGAGCAACCTCTAAAAGCAGTTTAGAGTGGTAAAAAA

## **FIGURE 58**

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMI FIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMAQ

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

### **Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

### **N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216



## **FIGURE 60**

MVGAMWKIVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL  
VGPFPGGLNMKSYAGFLT VNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLDRDRDPFWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQT  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHS LNPFVREV KINLNGIAIGDGYSDPESIIQG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVGT  
CSNYYNFLRCTEPEDQLYYVKFSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIIYNGQLDII VAAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIQR  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDPPYVG

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

### **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

### **Tyrosine kinase phosphorylation site.**

amino acids 423-432

### **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

### **Serine carboxypeptidases, serine active site.**

amino acids 200-208

### **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAAGTCTTGTGGCTACAACAT  
TTTTCCCTTTCCTAACAGTTCTAACAGCTGTCTAACAGCTAGTGATCAGGGGTTCCTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACAGCTCCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCTGCGCTAACAGCTTTCAAAAACAGGAGCGACTTCCACTTGGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCTTAATATCAAATTGACTGGCTGGG  
TGAACCTTCAACAGCCTTTTAACTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTTGTAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCCTAAGAGGGAGAAAGTATGTTAAAAATA  
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCCTGGGT  
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTAATTTTGGTCTGACCACTCTGCCTTGTGTTTT  
GCAGAATCATGTGAGGGCCAAACGGGGAAGGTGGAGCAGATGAGCACACAGGAGCGCTCT  
CCTCACCGCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG  
ACAGCCGCTTGTGGTCTGTCTCTCAGTGGTCTGGGTGCTCTGGCCCCCCAGCAGCCGGC  
ATGCCTCAGTTTCAGCACTTCCACTCTGAGAATCTGACTGGACCTTCAACCACTTGACCGT  
CCACCAAGGGACGGGGCCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAGAGGACAACAAGTCTCGTTACCCG  
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTACCCCTCACCAACAATGTCACAACAGCTGCT  
CATCATTGACTACTCTGAGAACCCTGCTGGCCTGTGGGAGCCTCTACCCAGGGGCTGTGCA  
AGCTGCTGCGGCTGTGATGACCTCTCATCTCTGGTGGAGCCATCCCAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCCTGTCCA  
GCCGAAGCTGCCCGAGACCCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCTTGGCCCTGGTCTCCCACTTTGACAT  
CTTTACATCTACGGCTTTGTCTAGTGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTTCTACACCTCACGCATCGTGGCG  
CTCTGCAAGGATGACCCCAAGTTCACCTCATACGTGCTCCCTGGCCCTCGGCTGCACCGGGC  
CGGGGTGGAATACCGCTCTCTGCAGGCTGCTTACCTGGCCAGCCTGGGGACTCACTGGCCC  
AGGCCTTCAATATCACCGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAA  
CAGTATCACCAACCCGCCCCGATGACTCTGCCCTGTGTGCTTCCCTATCCGGGCCATCAACT  
GCAGATCAAGGAGCGCTTCAGTCTGTCTACCAAGGGCAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGGAAGGACGCTCCAGTGCACGAAGGCGCTGTCCCATCGATGATAACTTCTGTGGA  
CTGGACATCAACGCGCCCTGGGAGGCTCAACTCAGTGGAGGGCCTGACCTGTACACCA  
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTT  
TGGGGATCAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTTCAGATGCTCCCAATGCC  
ATTCACTCTCCTCAGCAAGAGTCCCTCTTGAAGGTAGCTATGGTTGGAGATTTAATATAG  
GCAACTTTATTTTCTTGGGGAACAAAGGCTGAATGGGAGGTAAGAAGGGGTAAATTTTGTG  
ACTTAGCTTCTAGCTACTTCTCCAGCCATCAGTCATTGGGTATGTAAAGGAATGCAAGCGTA  
TTTCAATATTTCCCAAACTTTAAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAA

## **FIGURE 62**

MGTLGQASLFAPPNGYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLTTAAPLSMEQRQPWP  
RALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL  
YQGVCKLLRLDDLFIIVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPRDPRESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASSGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFAIFSKGQKYHHPPDDSALCAFFIRAINLQIKERLQSCYQGEEN  
LELNWLLGKDVQCTKAPVIPDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKKVRVYEFRCNSAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

### **Signal sequence:**

amino acids 1-32

### **Transmembrane domain:**

amino acids 71-87

### **N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

### **Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

### **N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCC GCGCGCGCTGAGTGC GGA CTGGAGTGGGAACCCGGGTCCCCGCTTAGAGAAACGCGCATGACCA  
CGTGGAGCTCTCCGGCGGAGGCGCGCCGCA CGCTGGGACTCTGCTGTGTCGTCTGGTCTCTGCTGTGCTCTC  
GCAGGCTGGACTGGAGGACCCCTGTGTCCTCTCGCGCTCCGCGCATGCAGACGTGGGGCTCAGGCCAGGCGGAGTACT  
ACTTCATGCTGGAGGATTCACCTTCTGGATCTTCGGGGCTCCATCCACTATTTCTCGTGGCCAGGAGTACT  
GGAGGGACCGCCTGCTGAAGATGAAGGCTGTGGCTTGAACACCCCTCACCACCTATGTTTCGTGGAACTGTGAT  
AGCCAGAAAGGCGAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCTCTGCTCTGGATGGCCCGCAGAGATG  
GGCTCTGGGTGATTCTCGCTC CAGGCCCC TACATCTG CAGTGGAGATGGACCTCGGGGGCTTCGCCAGCTGGCTAC  
TCCAAGACCTGGCATGAGGCTGAGGCACTTA CAAGGGCTTCA CCGAAGCAGTGGACCTTTATTTTGACCACC  
TGATGTCCAGGGTGGTGGCTCCTCAGTACAAGCGTGGGGGACTATCATTGGCTG CAGGTGGAGATGAATATG  
GTTCTCTAATAAAGACCCCGCATACATGCCCTACGTCAAGAGGCACTGGAGGACCGGTGGCATTTGTGGAACCTGC  
TCCTGACTTCAGACAACAAGGATGGCTGAGCAAGGGGATTTGTCCAGGGAGTTGGGCCACCATCAACTTTCAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTC CAGGGGAGCTCAGCCCAAGATGGTGTATGGAGT  
ACTGGACGGGTGTTGTTGACTCGTGGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTGTGAAAACCGGTG  
CTGCCATTGTGGACGCGCGCTCTCCATCAACCTCTACATGTTCCACGGAGGCCAACCTTTGGCTTCATGAATG  
GAGCCATGCACCTCCATGACTACAAGTCAGATGTCA CAGCTATGACTATGATGCTGTCTGACAGAAGCCGGCG  
ATTACACGGCCAAGTACATGAAGCTTCGAGACTCTCTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
ACCTTCTTCCCAAGATGCCGATGAGCCCTTAA CGCCAGCTCTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC  
TGGGGGAGCCAAATCAAGTCTGAAAGCCCATCAACATGGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCT  
TCGGGTACATTTCTCTATGAGACCGACATCACTCGCTTGGCATCTCAGTGGCCACGTGCATGATCGGGGGCAGS  
TGTTTGTGAACACAGTATCCATAGGATCTTGGACTACAAGACAACGAAGATTGCTGTCCCTCTGATCAGGGTT  
ACACCGTGTGAGGATCTTGGTGGAGAATCGTGGCGAGTCAACTATGGGGAGAATATTGATGAC CAGCGCAAAG  
GCTTAATTGGAATCTCTATCTGAATGATTCACCCCTGAAAAACTTCAGAAATCTATAGCTGGATATGAAGAAGA  
GCTTCTTTCAGAGGTTCCGCCCTGGACAATGGNGTTCCCTCCAGAAACCCCACTTACCTGCTTCTTCTTCTGTG  
GTAGCTTGTCCATCAGCTCCA CGGCTTGTGACACCTTTCTGAAGCTGGAGGCTGGGAGAGGGGGTGTATTCA  
TCAATGGCCAGAACCTTGGAGCTTACTGGAACATTTGGACCC CAGAAGACCTTTACCTCCAGGCTCCCTGTGGTTGA  
GCAGCGGAATCAAC CAGTTCATGTTT TTAGGAGAGCATGGCGGGCCCTGCAATTAAGCTTCACGGAAACCCCC  
ACCTGGG CAGGAAC CAGTACATTAAGT GAGCGGTGGCAACCCCTCTCTGTGGTGCATCTGAGAGCTGCCGCTC  
CTCTTGACCTGAAGCTGTGGCTGTCTGCCCAACCCCTCACTGCAAAAGCATCTCTTAAGTGAACCACTCAGG  
ACTGGGGCTTACAGTCTGTGCTCTCAGCTCAAAACCCCTAAGCTG CAGGGAAGGTGGGATGCTCTGGGGCT  
TGGCTTTGTGTGATGATGCTTCTTACAGCCCTGCTCTTGTGCCGAGGCTGTGGGCTGTCTCTAGGGTGGGAGC  
AGCTAATCAGATCGCCCACTTTGGCCCTCAGAAAAAGTGTGAAAGCTGCCCCCTG CACC CGGACGTCA CAGCCC  
TGCAGCATCTGCTGACATCAGGCGTCTCTTTGTCTGTGTTCTGGGAGGCTGGGCCACATCCCTCATGGCCCCAT  
TTTATCCCCGAATCTCGSGTGTGTCAC CAGGTAGAGGGTGGGGAAGGGGTGTCTCACTTGAGCTGACTTTGTT  
CTTCTCTCAACACCTTCTGAGCCCTCTTTGGGATTCTGGAAGGAACTCGCGGTGAGAAACATGTGACTTCCCTT  
TCCCTTCCACTCGCTGCTTCTCCACAGGTTGACAGGCTGGGCTGGAGAAACAGAAATCTCACCTCGCGCTCTCC  
CAAGTTAGCAGGTGTCTTGTGTTCTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA  
CATCCAGGGAGGAGCAGAGAGGCC CAGCTCACATGTGAGTCTCTGGCAGAAGCCATGGCCCATGTCTGCACTCC  
AGGAGGAGGAGCAGAGAGGCC CAGCTCACATGTGAGTCTCTGGCAGAAGCCATGGCCCATGTCTGCACTCCAGGAG  
GGAGGACAGAGGCC CAGCTCACATGTGAGTCTCTGGCAGAAGCCATGGCCCATGTCTGCACTCCAGGAGGAGG  
ACAGAGAGGCC CAGCTGAGGCCCGCTTCCCAACCCCCACGCCGGAACAGCAGGGGGCAGAGCAGCCCTCTTCT  
GAAGTGTGTCAGTCCGATTTGAGCCTTGTCTGGGGCC CAGCCCAACCTGGCTTGGGCTCACTGTCTGTA  
GTTGCAGTAAAGCTATAACCTGAAATCAAA

00000000.00000000

## **FIGURE 64**

MTTWSLRRRPARITGLLLLLVVLGFLVLRRLDWSITLVPLRLRHRQLGLQAKGWNFMLEDSTFW  
IFGGSIHVFRVPREYWRDLRLKMKACGLNTLTITYVPWNLHEPERGKFDMSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTAEVDLYFDHLSRVVPLQ  
YKRGGPIIAVQVENEXGSYNKDPAYMPYVVKALEDRGIVELLTSDNKDGLSKGIVQGVLAT  
INLQSTHELQLLTTFLFNVQGTQPKMVMYWTGWFDSWGPHNILDSSSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAHYMKLRDFFGSISGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFYIILYE  
TSITSSGILSGHVHDRGQVFVNTVTSIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSPKFNFRYISLDMKKSFFQRFGLDKWXSLEPETPTLPAPFFLGSLGIS  
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

### **Signal sequence:**

amino acids 1-27

### **Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

### **N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586



## FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGGCTCGGCCGAGGCCCCAGGACCTCATCTCCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGAAACGCCATGGCTCCC  
AAGAAGCTGTCTGCCTTGGCTTCCCTGCTGCTGCCGTCAAGCTACTGCTGTGCCCA  
GGCAGACACTCGGTCTTCTGTAGTGGATAGGGGTATGACCGGTTTCTCCTAGACGGGGCCC  
CGTTCCCGCTATGTGTCTGGCAGCCTGCACCTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC  
CGGCTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGGTCTATACTTTAATGGCAGCCGGGACCTCATTCGCTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG  
TGGGAGATGGGGGCTCTCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC  
AGATCCAGACTTCTTTCGCCGAGTGGACTCCCTGGTTCAAGGTCTTGTCTGCCCAAGATATATC  
CATGGCTTTATCACAATGGGGCAACATCATTAGCATTCAAGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCCTGTAGG  
AGAAAAGATCTTGTCTCTTACCACAGATGGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATACCAGCTAGATTTTGGCCAGCTGACACACATGACCAAAATCTTTACCTCGCTT  
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG  
AATGTTGCCGATAAGAAGGGACGCTTCCCTCCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTGCTCTTCAGATGTCATCAGCAAGT  
TCCAGGAAGTTCCCTTTGGGACCTTTAACCCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCAT  
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATTGGCTTCATGTTGTACC  
GAACCTATATGACCCATACCATTTTGTAGCCAAACACCATTCTGGGTGCCAAATAATGGAGTC  
CATGACCGTGCCATGTGATGGGTGGATGGGGTGTTCAGGGTGTGTGTGGAGCGAAATATGAG  
AGACAAACTATTTTGAACGGGAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG  
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATCTG  
GGGCAACAATCCTTACCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTTCCCCCTCCAGTTGCCAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT  
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACTTGGGCCGTACTGGACAAAGCAGGGGCC  
ACAACAGACCCCTCTACGTGCCAAGATTCTGCTGTTTCTTAGGGGAGCCCTCAACAAAATTA  
CATTTCTGGAACCTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTTTGACAGGACACATATCAATTCCTTTTCAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAACTGGGCACCTGAAGGATAGGCCGGGCATGGTGGCTCATGC  
CTGTAATCCAGCACCTTTGGGAGGCTGAGACGGGTGGATTACTTGAGGTGAGGACTTCAAGA  
CCAGCCTGGCCAAACATGGTGAAACCCGCTCTCCACTAAAAATACAAAAATTAGCCGGGCGTG  
ATGGTGGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATTC  
AGGAGGCAGAGGTTGCAGTGAAGGTGTACACTGCATCTCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSVMRHLAGLFRALLGEKILLFTTDDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYTTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMFMFHGGTNF  
GYWNGADKKGRFLPIITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGLKLSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDFTLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

### **Signal sequence:**

amino acids 1-27

### **N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

### **Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

### **Tyrosine kinase phosphorylation site.**

amino acids 191-198

### **N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGCCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTTATCTGCCTCTACACTCTTCTGTTATTTCAGGATACCTTTGAAGGAATATT  
CTTTGCAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT  
GCGTTCTCTTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT  
CTTGTCAGAAGTTAGTGAAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG  
CTGTGCGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA  
TGCCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTTCATAATGACGGCAC  
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA  
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAAGCTGGAT  
TTAAAGTCCAATAACATTGCGACAATTGAGGAAATCATCAGTTTCCAGCATTTAAACGACT  
GACTTGTTTAAAAATTATGGCATAACAAAATTGTTACTATTCTCCTCTATTATCCCATGTCA  
AAAAGTTGGAGTCACTTTATTTCTTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT  
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGTCATATCACTGGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAAGCTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAAGCTG  
CTTGGAACCGCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTTG  
TGGAAGATCACCTTTTGTACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCTTTGCAAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AATCTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG  
ATACATCTTTTAAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTTGTAGGGTTTTAAGTCATTTCATAATCATTTTTTTTTTTCTTTTGGGG  
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTTAAATGTTTGTAACTTGGAT  
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKLLISYISIIICVYGFICLYTLFWLFRIPLEKEYSEFKVREESSFSDDIPDVKNDFAFLLHMVDQYDQLYSKRFGVFLSEVSENKLEISLNHEWTFEKLKQHISRNAQDKQELHLFMLSGLVPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLHKVFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESRLRELRLKILHVKSNNLTQVPSNITDVAPHLTKLVIHNDGTLKLLVLNSLKKMMNVAEELQNCCELERIPHAIFSLSNLQELDLKSNNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESILYFSNNKLESPLVAVFSLQKLKRLDVSNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLNGQNCITSLPEKVGQLSQTQLLELKGNCLELRLPAQLGQCRMLKKSGLVVEDHLFDLTLPLEVKEALNQDINIPFANGI

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

### **Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

### **Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

### **N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCCACGCGTCCGGCCTTCTCTCGGACTTTCGATTTCATTCCATTCTTTTCATTGACAACTGACTTTTATTTATTTCT  
 TTTTTCATTCTCTGGGCCAGCTTTGGGATCCTTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT  
 CTGTGTTTGGGGTTTCTTCTTCCCTCGACATTTGGCATTGCTTAGTGTTGTGTGGGGAGGGAGACACGTTGG  
 GCTCAGTCTTTGCTTGCACCTTATCTGCCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGTATGCTCCTGTC  
 ATCGCTGGTGGTATCTCGGCCCTTGTCTCTGTGATAGTTGTCTGTCTCTTTACTTCAAATAACACAAAC  
 GCGCTAAAGAGCTGAAAAGAACTGAAGCTGTGGCTGTAAAAATACAAACCAGACAAAGTGTGGTGGGCCAAG  
 AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCCCTCAGTGTCTGTGAAGGATATAGAATGTGTGCC  
 AGTTTTGATTCCCTGCCACTTGTCTGTGCGACATAAATGAGGGCCTCGAGTTAGGAAAGGCTCCCTTCTCAA  
 GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTGTGATGTGCGAGGCACAGAAAGAGGCACAG  
 CTCCCATCAGTTTTCATGGAAAAATACTCAGTGCCTGCTGGGAACCAAGCTGCTGAGATCCCTACAGAGAGCTTC  
 CACTGGGGGCAACCCTTCCAGGAAGAGTGTGGGAGAGAGAACCTCACTGTGGGGAATGCTGATAAACAGCTCA  
 CACAGCTGCTTATCTCACACAAATCTACCCCTTGCCTGTGCTGGAACCTGACCTTCCCTGGAGGTGCCAGAAA  
 GCTGATGTAAACAGAGCCTATAAAAGCTGTCTGGTCTTAAAGCTGCCAGCGCCTTGCCAAAATGGAGCTTGT  
 AGAAGGCTCATGCCATTGACCTCTTAATTCTCTCTGTTTGGCGAGGCTGACAAATGGCGGAGGCTGAAGGCAAT  
 GCAAGCTGCACAGTCACTTAGGGGGTGCCAAATATGGCAGAGACCACAAAGCCATGATCTGCAACTCAATCCC  
 AGTGAGAACTGCACCTTGGACAAATAGAAAGACCAGAAAAACAAAGCCATCAGAAATATCTTTTCTCATGTCCAGCTT  
 GATCCAGATGGAAGCTGTGAAAGTGAAACATTAAGTCTTTGACGGAACTCCAGCAATGGGCCCTCTGCTAGGG  
 CAAGTCTCAGTAAAAACGACTATGTTCTCTGATTTTGAATCATCATCAGTACATTGACGTTTCAAATAGTTACT  
 GACTCAGCAAGAATTCAAAGAACTGCTTTGTCTTCTACTTCTTCTCTCTCAACATCTCTATTCCAAACTGT  
 GCGGGTTACCTGGATACCTTGAAGGATCCTTCCACAGCCCCAATTACCAGGCGCATCTCTGAGCTGGCTTAT  
 TGTGTGTGGCAGACATAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCCATGAAATAGAC  
 AAACAGTGCAAAATTGATTTTCTTGGCATCTATGATGGCCCTCCACCAACTCTGGCTGATTTGGACAAAGTCTGT  
 GGCGGTGACTCCACCTCGAATCGTCATCAAACCTCTGACTGTGCTGATCAGATATGCGCAATTCT  
 TACCGGGGATTTTCTGCTTCTCACTCACTCAATTTATGACAGAAACATCAACACTACATCTTTAACTTGTCTCTCT  
 GACAGGATGAGAGTTATTATAAGCAATCTTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCACATAAAA  
 GACCCAACTTGCAGACCAAAATATCAAATGTGTGGAATTTTCTGCTCTTAAATGGATGTGGTACAACTCAGA  
 AAGGTAGAAGTCAAGTCAATTACTTACACCAATATACTCACTTTTCTGCTCTCAACTCTGAAAGTGTACACC  
 CGTCAGAAACAACTCCAGATATTGTGAAGTGTGAAATGGGACATAATCTCAGTGGAGATAATATACATAACA  
 GAAGATGATGTAATACAAAGTCAAATGCACTGGGCAATATAACACCAAGCATGGCTCTTTTGAATCCAATTCA  
 TTTGAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACAAAACCTCTTTTGTCTCAAGTTAGTCTGCAC  
 ACCTCAGATCCAAATTTGGTGGTGTCTTGTGATACCTGTAGAGCCTCTCCCACTCTGACTTTGCACTCTCCAACC  
 TACGACCTTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAGGTGTATCCCTTAATTTGGACATATGGGAGA  
 TTCCAGTTTAAATGCTTTAAATCTTGAAGATATGAGCTCTGTGTATCTGCAAGTGAAGTTTGTATATGTGAT  
 AGCAGTAGACCAACAGTCTGCTGCAATCAAGTTTGTGTCTCAGAAAGCAACGAGACATTTCTCATATAAATGG  
 AAAACAGATTTCCATATGAGACCACTTCTGTGAAAGGGATCGAAGTGGCAAGTGGCAATTCAGGATTTTCAGAT  
 GAAACACATGCGGAGAACCACTCCAAACCAGCCTTTCACAGTGTGCACTGTGTTCTTCTCATGGTTCTAGCTCTG  
 AATGTGGTGACTGAGACCAATCAAGTGGGCAATTTGTAAATCAACGGGCAGACTCAAAATACCAAGAGCTG  
 CAGAACTATTAACTAAACAGTCTCAACCCCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCTG  
 GGCTACACATATTATGAATAAATGAGGAAGGCCCTGAAAGTGACACAGGCGCTGCATGTAAAAAA

## **FIGURE 70**

MELVRRLLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSIVQLDPDGSCESENIKVFDTSSNGPLLGQVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSTSPNYPKHPPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVPTPFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVVISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVFEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIYYITEDDDVIQSNALGKYNTSMALFESNSFEKTILESPYYVDLNLQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDPASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAPKFLRSMSSVYL  
QCKVLICDSSDHQSRNCQGCVSRSKRDISSYKWKTDSEIIGPIRLKRDRSASGNSGFGHETHA  
EETPNQPFNSVHLFSFMVLALNVVTATITVRHFVNQADYKYQLQNY

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domain:**

amino acids 571-586

### **N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

### **Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

### **N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGCTG  
TGCTGCGCCGCGCCGCGTGCCTGCCACAGCGCCACGCGCTTCGACCCCACTGGGAGTCC  
CTGGACGCGCCGCGCAGCTGCCGCGTGGTTGACCAGGCCAAGTTCCGGCATCTTCATCCACTG  
GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA  
AGATACCGAAGTATGTGGAAATTTATGAAAGATAATTACCCCTCCTAGTTTCAAATATGAAGT  
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAAGTGGGCAGATATTTTTCAGGC  
CTCTGGTGCCAAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT  
CAGAATATTCGTGGAAGTGAATGCCATAGATGAGGGGCCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTGGAGCTGTACTATTCCCTTTTGA  
ATGGTTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT  
ATATAATGAAAGCCCAGTTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA  
CATAAATGGGAAAAGTGCATGACAATAGACAAAGCTGCTGGGGCTATAGGAGGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAAATGGTGAAGCAACTTGTAGAGACAGTTCATGTG  
GAGGAAATCTTTTGATGAATATTGGGGCCCACACTAGATGGCACCATTCTGTAGTTTGTGAG  
GAGCGACTGAGGCAAGTGGGGTCTTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT  
CCCCAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGGCCATTTAACTG  
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAAACCATTATCAGATGC  
CGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGAAACTGGATAAGAAAATTAATTGGCAGTTACGCCCTTCCCTTTTCCCACATA  
AATTTTTCTTAAATTACCCATGTAAACATTTTAACTCTCCAGTGCACTTTGGCATTAAAGTC  
TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCACATTATAGTAG  
CAAGGAATTTGGTGGTATTATGGACCGAACTGAAAATTTTATGTGTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCACTCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT  
TTTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAAACTGTAAAAATAAATGGTGCACCTGTATAGGCACTTACCACGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGGTGAAGTCAAGTGAAGTGAATGGAAGGCTAGGACATTA  
TTGAACACTCGCCAGCGTTATAAATACCTGTATGCTTAGGCTACACTACATTTTATAAAAAAAA  
GTTTTCCTTTCTCAATTATAAATAAACAATAAGTGACTGTAACTTTTACAAAGCTTTTAAATT  
TTTAAACCTTTTGGCTCTTTTGTAAATAACACTTAGCTTAAACATAAACTCATTGTGCAA  
ATGTA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPWTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRDRLRFGLYSLFEW  
FHPFLFEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVNTDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVTPDVWYTSKPKKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

### **Signal sequence:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

### **Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

### **Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

### **N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

### **Leucine zipper pattern.**

amino acids 410-432

### **Alpha-L-fucosidase putative active site.**

amino acids 283-295



## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
 TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC  
 TGAGGTGTTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG  
 CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT  
 TTCCATCCAGGTGTCTATGCAGAATTATGGGGATCACCTTGTGTAGCAAAAAGGCCAAGC  
 AGCTGAATTTACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG  
 GACCAAGTTGAAACAGCCTTGAAGAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA  
 TGGATTGCTGGTCACTCTTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
 TCCTGATTTGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT  
 ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATTATCAACACTCA  
 AACTGCAACACAAACAACAGAAATTATGTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT  
 ACTCTACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTTCCACGG  
 AGAAAAAATTGATTGTGTGCAGAGAAGTTTTTATGGAACTAGCACCATTGTCTACAGAAAC  
 TGAACCATTTTGTGAAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC  
 CCACGGCTCTGCTAGTGCTTGCTCTCTCTCTCTTGGTGCTGCAGCTGGTCTTGGATTTTGC  
 TATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT  
 CGAAACCAAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA  
 AAACGTGATAAAACCAGAAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGCCTGGAA  
 GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACTGAGGCTGGTTTTCTTATGCTCC  
 TTACCTTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAGAAAGTCCACCCTT  
 GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGACCAAAGAGAAATGC  
 CCTTCTCCTTATTGTAAACCTGTCTGGATCCTATCTCTCTACCTCCAAAGCTTCCACGGCC  
 TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGCAA  
 GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCTGGCTGTCTGAGGCTAGG  
 TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATCCGCAGCTCAGAC  
 CCTTCTTCAGCTCTGAAAGAGAAAACCGTATCCCACCTGACATGTCTTCTGAGCCCGGTA  
 AGAGCAAAAGAATGCGAGAAAAGTTTAGCCCCGAAAGCCATGGAGATTCTCATAAAGTTGAG  
 ACCTAATCTCTGTAAGAGTAAAATAAGAAATAGAAACAGGCTGAGGATACGACAGTACACT  
 GTCAGCAGGGACTGTAAACACAGACAGGCTCAAAGTGGTTTTCTCTGAACATTGAGTTGGA  
 ATCACTGTTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCT  
 AGGAAATATACTTTTACAAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTATCTGA  
 GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTTAAAAAGTAATAAAATTCA  
 ACAACATTTTCTGTAATGACTACTATATGTCAAGTGTCTGTGCAAGGTATTACACTCTGTAAT  
 TGAATATTATCTCTAAAAAATGACATAGTAGAACGCTATCTGGGAAGCTATTTTTTCA  
 GTTTTGATATTTAGCTTATCTACTTCCAACTAATTTTATTTTGTCTGAGACTAATCTT  
 ATTCAATTTCTCTAATATGGCAACCATTTATAACCTTAAATTTATTTAACAATACCTAAGAAG  
 TACATTGTACCTCTATATACCAAAGCACATTTTAAAGTGGCAATTAACAATGTACTACTA  
 GCCTCTCTTTTCCAAACAAGAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA  
 AGCATTTTAGAAAACCT

## **FIGURE 74**

MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPVSRQF  
AAYCYNSSDTWTNSCIPEIIITTKDPIFNTQTATQTTFEFIVSDSTYSVASPYSTIPAPTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETETPFVENKAAFKNAAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPTNKNQKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSP  
SKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTCCGTGCCGCGACTTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGTGCGCTTCTCTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGTCTGCCCCACCCAAACGCGAAGACGGTAACCCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCCGAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT  
TCTTTTCTTCCGCTTGGATATTGCGATGGGCCCTACTTTACATCACACTCTGCATAGTGTTC  
TGATGACGTGCAAAACCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATGTATGAGGAAC TAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCCTTTGCCAA  
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC  
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC  
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCGTGATCCTGTTCCTCAAGGTGGCAA  
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG  
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA  
TGGGGAAAAAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGTCTCCTCTCCTGTCAATT  
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG  
CTGNACTGGNTGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG  
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAACGTGTTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGAAATGGTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC  
AGCTATTGACACATCTCCATGGTTTCTCCATGAACTCTGTGGTTTCATCATTCCTTCTTAG  
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGGTATAGAA  
CGCTAAGAATTTTCCCCAAGGACTCTTGCTTCTTAAAGCCCTTCTGGCTTCGTTTATGGTC  
TTCATTAAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG  
TTTTTTATCATTGAAGACAATTTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTTCCTTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCAC  
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCGTAATAAAAAGATTGGGATT  
TCCTTTTG

## **FIGURE 76**

MAVLAPLIALVYSPRLSRWLAQPYLLSALLSAAFLLVKLPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTI DEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN  
TGLNFGKVDVGRYTVDVSTYKYSTPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

### **Signal sequence:**

amino acids 1-48

### **Transmembrane domain:**

amino acids 111-125

### **N-glycosylation site.**

amino acids 165-169, 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

### **N-myristoylation site.**

amino acids 188-194, 225-231

### **Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

**FIGURE 77**

[illegible]

## **FIGURE 78**

MGLLLLVLPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRRYREPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPQPCGGPGLAPGVRSYGPR  
HRLHRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPNCGPPEPGVRSFGFPDQSRLYGVICYRQH

### **Signal sequence:**

amino acids 1-17

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

### **Tyrosine kinase phosphorylation site.**

amino acids 137-145

### **N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC  
TTCGTGTGCTACTGAGGCAAGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAAGGCGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACAGGGAA  
CTTCAGTACGACCATGAGGCTTTCCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCCCGTCTGGGGCGGATCGTGGACCGCATGGAACCGCGCGGGGAC  
GGCGACGGCTGGGTGTGCTGGCCGAGCTTCGCGCTGGATCGCGCACACGCAGCAGCGGCA  
CATACGGGACTCGGTGAGCGCGCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG  
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCCGGTGAAGAATTTTCATGAC  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGCGCTTTCGGGTGGC  
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG  
AGTTCCCTCACATGCGGGACATCGTGATGCTGAAACCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA  
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCGGGACTTCCGGGATCTGAACAAGG  
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCAGCCC  
CTGGTGGAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA  
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCCG  
CACAATGACCGGAGGAGGGGCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGCAGGAG  
GCAGATGCAGTCCCAGGCATCCTCCTGCCCTGGGCTCTCAGGGACCCCTGGGTGCGGCTTC  
TGTCCTGTGCACACCCCAACCCCAAGGGAGGGGCTGTGCATAGTCCAGAGGATAAGCAATAC  
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTTGCCCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCAGCTCCAATCTGAGCCTCCACCACATAGACTGAAACTCCCTT  
GGCCCCAGCCCTCTCCTGCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA  
AAGCCAGCGCCGGGACCTTGAAA  
AAAAAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLLLLRHGAQKGKPSFDAGFHGQGRVHQAAPLSDAFHDDAHGNFYDHEAFLGR  
EVAKEFDQLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSDMATRE  
ELTAFLHPPEEPPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAAWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHVLPAPAQDQPLVEANHLLHESDTPDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 140-144

### **Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

### **N-myristoylation site.**

amino acids 263-269, 311-317

### **Endoplasmic reticulum targeting sequence.**

amino acids 325-330



## FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
 GCGGCGGGCGCGGGTGCAGAGGGATCCCTGACGCCCTCTGTCCCTGTTTCTTTGTCGCTCCACG  
 CCTGTCTGTGTCGTTTGGCGCCCCCGCTCCCGCGGTGCGGGGTTGCACACCGATCCTG  
 GGCTTCGTTCGATTTGCCGCCGAGGCGCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
 CGGGTCGTCTGTGTCCTCTCTCCTCTGCGCGCGCCCGGGGATCCGAAGGGTGCGGGGCTCT  
 GAGGAGGTGACGCGCGGGGCTCCCGCACCTGGCCTTGCCCGCATTCTCCCTCTCTCCAG  
 GTGTGAGAGCCTATCAGTCACCAATGTCCCGAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG  
 TGTCTGCTGCTGTCGGGGGCCCGCGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG  
 TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCCAGGGGGCTGCC  
 CTCTTGAGGAATTTCTCTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
 GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC  
 TGGTCGAGAAAATATTTCTCAGTAGATGCCAATGGCATCCAGTCTCAAAATGCTTTCTAGAT  
 GGTCTGCTCTTTACAGTAACATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
 GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACCCGAGAGAAGAACTGG  
 CAATAAAGATTGTAAAGCAGACATTCGATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC  
 GCCGATTTAATTTACAGAAGAAATTTGTTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA  
 GAAGGACCACATGTGGGCCTTGTTCAAGCCAGTGAACATCCCAAATAGAATTTTACTTTGAA  
 AAACCTTACATCAGCCAAAGATGTTTGTGTTGCCATAAAGGAAGTAGGTTTTCAGAGGGGGTA  
 ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTTCTCACGGTAGATGCTGGA  
 GTAAGAAAAGGGATCCCCAAGTGGTGGTGGTATTATTGATGGTTGGCCTTCTGATGACAT  
 CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA  
 AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT  
 CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA  
 GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
 CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGTGAGATAGCAATTTCCGCCCTC  
 ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAATCTCGGACATTGGTGCCAAGAT  
 AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAAGTTTCACTGACTATAGCACC  
 AAGAGAATGTCCTAGCTGTATCAGAAACATCCGCTATATGATGGTGGAACAGCTACTGGT  
 GATGCCATTTCTTCTCAGTGTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCACAAGAA  
 CTTCTAGTAATTGTACAGATGGGCAGTCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
 CACATGATGCAGGAATCATTATCTTCTGTTGGTGTGGCTGGGCACCTCTGGATGACCTG  
 AAAGATATGGCTTCTAAACCGAAGGAGTCTCAGCCTTTCTTCAAGAGAGTTCAAGGATT  
 AGAACCAATTGTTTCTGATGTATCAGAGGCATTGTAGAGATTTCTTGAATCCCAGCAAT  
AATGGTAACATTTTGCAACTGAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTTGTAAT  
 CTCATAATACAGAAATGCTTTAGCATACTAGAATCAGATACAAAACTATTAAGTATGCTAAC  
 AGCCATTAGGCAAAATAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT  
 ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTTTAGAACTCAGGAAAGGGA  
 GATAATGTGGATTAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA  
 TTCATAGCTCAATAAAGAACTGATACTTAGACCAAAAAAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGCCPLEEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRRGNSNTGKAL  
KHTAQKFFTTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAPLI  
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTFEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVITDGGQSYDDVQGPAAAAHDAGITI  
FSVGVAWAPLDDLDKMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

### **Signal sequence:**

amino acids 1-24

### **N-glycosylation site.**

amino acids 100-104, 221-225

### **Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

### **N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

### **Amidation site.**

amino acids 145-149



## FIGURE 84

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSYQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEAEAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDSECCG  
DQLCVWGHCTKMATRGSGNTICDNQRDCQPLCCAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEEI

### Signal sequence:

amino acids 1-19

### N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

### Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### N-myristoylation site.

amino acids 202-208, 217-223

### Amidation site.

amino acids 140-144



## FIGURE 86

MRLLVAPLLLA W VAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTL LLQNSI VRVDQSELGYLANLT ELDLSQNSFS DARD CDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ  
LARVPRRALEQVPGKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSDKFPALVNLP  
ELTKLDITNNPRLSFIHPRAFPHLPQMETLMLNNA LSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVRVPPFREMTHDCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRRLTPAHAGRRYRVYPEGTLELRRVTAEEAGLYT  
CVAQNVLVGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW  
SSASSLRQGQATALARLPRGTHSYNITRLQATEYWA CLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGRRPLPPAWAFWGSAPSVRVV  
SAPLVLPWNPGRKLPRSGEETLLPPLSQNS

### Signal sequence:

amino acids 1-18

### Transmembrane domain:

amino acids 629-648

### N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

### Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

### Tyrosine kinase phosphorylation site.

amino acids 532-540

### N-myristoylation site.

amino acids 15-21, 493-499, 566-572

### Amidation site.

amino acids 470-474, 660-664, 692-696

[illegible]

CAACGACGAGCGCGCTTTTGAAGAAGTGAAGAAGTTCCGGACCAACATGTGGAGGAGGGGGACATGTGTGACCGCCT  
CTATCGCGGACAGACATCATCAAGTGTCAAGTTCTCCCTCATCATCTGTGTACACCGCTCTATCATCGGTGACAA  
CATCAAGTTTGACATGSGATCTGACCGTGGACATGTAGAGACCTGAGCGGCTACCGACCTACCGGCTGCGCCACC  
CTGGCGACACATCTTCAAGATCTGGCGCTCTCTTCTACATCAGCTAGTCACTTCTTACGCGCTCATCTGTCAATGTA  
CACATCTGTGGTGGATGTGATCGCGCGCTCCCTCAAGAAGTACTCGTGTGAGTCGATCCGTGAGGAGACAGCTACAG  
CGACATCTCCCGACGATCAAGAACGACCTTCCGCTTCTATGTCACCTCATATGACCAATCGACCGCCTCTATCTCCA  
CGCCTTTCGCGCTTCTCTGTTCGGAGGTGAGTGAGAACAGCTCGCGACGCTGAACCTCAACACAGAGTGAGCGCT  
GGACAGATCTCGCGACCGGCTCACCAGAACGCGCAGAGACAGCTGGAGCTGACCTGTTCTATGTCTCTCAAGTGGCT  
CCCTGACACTGTGTTTGAAGCTGGTGGAGCTGGAAGTCTCAGAGTGGAGTCTGATCCCGACGTGACACCTCCGCG  
ACGATTTCCGACGATCACGGGCTCAAGGACTGTGGCTTACCAACACAGCGGCCAGAGTTTGAAGCGCTGCGCT  
GGCTTCTCTGCGAGAACTCGCGGCGCTGACATCAAGTTACGCGATCAAGGAATCCGCTGTGGTGTATCTA  
TAGCTTGAAGACATCTGGAGAGCTGACATCTGACGGGCACTGAGCGGGAGAACACCGCTATCATGTCTATCGA  
CGGGCTCGGGAGCTAAACCGCTCAAGTGTCTGGCTCAGAGACAGCTTAAGCAAGCTGTCCACAGAGTGTGTCA  
AGATGTGGGGCTGACCTCGACGAGGTGTCCATCAATCAATGAGGGACCAAGCTCATCTGCTCTCAACAGCGCTCAA  
GAAGATGGCGAACTGACTGAGCTGGAGCTGATCGCTGCGACCTGGAGCGACTCCCCACTCATCTTCAAGCT  
CAACAACTCTGACGAGATGAGCTCAAGCAACAACTCAAGAACATCAGGAGAGATCATCAAGCTTCTCAGCAACT  
GCACGGCTCAGTGCCTTGAAGCTGGTGTAAACCAACTGCGCTACATCCCACTGAGATCGGCAACTCACCAA  
CTTGGAGCGCCTCTTACTCAAGCCGACAAAGATGAGAGAGATCCCCACCCAGCTCTTCTTACTCTGCGCAAGCTGCG  
CTACCTGACCTCAGCCCAACAACTGACCTTCTCTCGTGGCAGATCGGCTCTCTGAGAAAGCTCAGAAACT  
AGGCATCAAGCGCAACCGGATCGAGAGCGCTCCGTCGAGACTTTCAGTGGCGGAAGCTGCGGGCCCTGCAACT  
GGGCAACAACTGTCCGATCTGCTCTCGGCTCGGGTGGGCGAGCTGACAACTCTGACGCAAGTGTGAGCTCGGGG  
GACCGGCTGAGAGTGCCTGCTTGGAGCTGGGCGAGTGGCCACTTGTCAAGCGCAAGCGCTGTGGTGGTGGAGGA  
GAACTCTTCAACACTCTGCGACCTGGAGGTGAAGAGCGGCTGCTGAGGGCTGACAAAGCTGAGGCTCTGACGAG  
GCGGCCCCAGCAGCAGCAGCAGGACCGCTCGCCAGTCTCAGGCCCCGAGGGGCGAGCGCTAGCTTCTCCAG  
AATCTCCCGGACAGCAGGACAGCCTCGCGCTGGGACAGGACCTGGGCGCGCTGTGAGTCAAGCTGCGCAGAG  
GAGCAGATATCTGTGGGCTGTGGCCCTTCTTCTCTGAGACTCAGCTCCCGCAGGCGAGGCTGTGGAGGAG  
AGCAGCTCTCAAGAGCGCATTTTGGATATTCAGTGTCTCTCTCGGAGGCGAGCTGTGCTCCGACGGCGCTAG  
CTGCAACACAGAGGCTCTGGGACCTTCACTTATGTTCTGTTATTTATTTCTTCATCTCCCACTCTCTCTCATC  
AGATAATCTTATCATCTCCAAGAAATTTCAAGCCAGATGGAAGTGTTCAGGAAAGGTGGGCTGCTTCTTCCCT  
TGTCTCTTATTTAGGACGTGCGCGGGACTTAAACCCACTGGACTCAGCAGAGTGTCTCGGGCGAACAC  
CAATGGGACGCTACCCAGCAGCTGCGGGCTGGGCTCTCGGCTGGCGTCCAGGGGAGAGCAGGCGCTCAGCTGGA  
AAGGCGCAGCTGAGAGCTGTCTCTTCAAGTTTGTGGAGGTTTAGTTTGTGTTTTTTTTTTTTTTAAACAA  
AAACAACTTTTTTTTTAAAAAAATGTTGAAATGAGATGTTTGGGATATAAAGAGAAAAAAATCTAAAAAA  
AAAGAACACTAAACCGGCACTGAGTTGGAGTCTCAGGCGAGGTTGGCAGTTCTCTGTGCAAGACAGCCAGAGT  
TGAATCTGTGTTTCTTCTCCGGGCGCAGGCTGACGGTGTCTTCGGAATCTGTGTGAATCTCTGTGTCAGAGTT  
CTATTGTTCTCGGGAGGAGGTTTTTTTTGTTGTTTGTGTTTTTGGGTTTTTGGTGTCTGTTTTCTTCTCCCT  
ATGTTCTTTCGAGGCACTCATTTCTGTGGCTGTGCGGAGAGGAATGTTCTGAGACTCGCAGGAGGGAGGAG  
ACTCGGTTTGGCTATATCCCGATGAAGCGTGTCCATGCACTCCCTCTCTGCTGCTGCTGCTCTGCTCTCA  
CGCACAGTGTTAAGGAGCCAGAGAGCCATCTCGCCAGACTTGTGTTCCCGCTTCTCTGCGGACTGGGTTGT  
CAGTGGCCACCGCTGGCTCTGCTGCTGTCTCATCGACTGCTGCGCACTGCTGCTTCAAGAGAGCAGACATTA  
GAGGCTGTGTGGGATATGGGAGGTCGCCCTGGGAGGGCGAGGCTGTGTTCAAGACCGGTTCCCGTCTGGGCG  
CTGGAGTGCACAGGCCAGCTGGCAGCTGGTGTCTGGAAGCAAGCTGCTTTAGATCATCTGGGTCGCCACT  
AGAGAGGCTCCCGCTTTAGATCAATCAGCTGGACATGAAGCAGCTTTTAGAGTCTCTGCTTAAATGATATGT  
CATCCGCTGTGCTGCTCAATTGTGTTTTGTGGTGTGCTGATGATATATCTCAGAAATAATGACACTAG  
CCTCTGACCAACCTAAGACAAAATCTCGTTACATGTGGGCTGAACTTGTAGACTCGGTACAGTATCAATAAA  
ATCTATACAGAAAATAAAAAAA

## **FIGURE 88**

MRQTIKVIKFIILICYTVVYVHNKIFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMRLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLRTKNAQDKLEHLFMLSIGIPDTPVFDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLHYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI  
YSLKTLLEELHLTGNSLAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFO  
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFPQCRKLRALHLGNVQLSPLSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

### **Transmembrane domain:**

amino acids 51-75 (type II)

### **N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

### **Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

### **N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447



## FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCTGCGCTGCTGCTGGGCCTGAACGACGAGAGCTGTCAATGACT  
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACCTTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACACGGAACCACTGGCTCCAGGCTGCCAGTCTCTCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCATATGCCAAGGA  
CCTGGCTATGTGGCTTCAGACATGATGGTTCTCTGAAGACCTTCTTCAGTTGCCACAAG  
AATTCAGACAGTTCCATTCTACATTTTCTCAGAGTCCATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATTGACGAGGGACCATCAAGTGCAACTTTGCGGGGT  
TGCCTTGGGTGATTCCGGATCTCCCCTGTTGATTGCGGTGCTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTTCTCTGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT  
GATCATTTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACATAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTTGTCTTTGTCAGCGC  
CACGTGAGACACCTACAACGAGATGCCCTTAAGCCAGCTCATGAATGGCCCATCAGAAAGAA  
GCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCCTG  
GGTGCGGAAACTGAAGTGGCCAGAAGTGCTAAATTCACTGAGCTGAAGTGAAGGCCCTGT  
ACAGTGACCCATAATCTTTGGAACATCTGCTTTTGTCAAGTCTTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT  
TGGGCGACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT  
AATGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATGTCTCT  
GGAGGCAATTTGGAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT  
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVVDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGGPGSSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTICKNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE  
ATELWGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSELEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKCLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPFLPKFSQLKWKALYSDPKSLETSAFVKS YKNLAFYWILKAGHMP  
SDQGDMA LKMMRLVTQQE

### **Signal sequence:**

amino acids 1-25

### **N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

### **N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

[illegible]

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGAGTGCAGGAGGCGCGCGCTTATCAGGACCATGCGGCCGA  
CGGGTCATCAGTCGCGCATCGTGGGTGGAGAGGACGCCGAACCTGGGCGTTGGCCGTGGCA  
GGGGAGCCTCGCCTGTGGGATTCCCACGTATCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCAGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCCTACTACACCCG  
TTACTTCTGTATCGAATATCTATCTGAGCCCTCGTACCTGGGGAATTACCCCTATGACATTG  
CCTTGGTGAGCTGTCTGCACCTGTCACTTACATAAACACATCCAGCCCATCTGTCTCCAG  
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAGGTGCGCCATCATAAACA  
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG  
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCTT  
GGCCTGTAAACAAGAAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG  
GTCGGCCCAATCGGCCCGTGTCTACACCAATATCAGCCACCCTTTGAGTGGATCCAGAAG  
CTGATGGCCGAGTGGCATGTCCCAAGCCAGCACCCCTCCTGGCCACTACTTTTTCCCTCT  
TCTCTGGGCTCTCCACTCCTGGGGCCGGTCTTGAGCCTACCTGAGCCATGCAAGCTGGGGC  
CACTGGCAAGTCAGGCCCTGGTTCTCTCTGTCTGTGTTGGTAATAAACACATTCAGTTGA  
TGCCTTGCAAGGCATTCTTCAAAAAAATAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 92

MGARGALLALLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAE LGRWPWQGSRLRW  
DSHVCGVSLLSHRWALTAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVITYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDALP  
SPHTLQEVQVAIIINSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWGVCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

### **Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

### **N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

### **Amidation site.**

amino acids 33-37

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

### **Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCCTAGGGCT  
 CTTTGGCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCCGACCAGCGGAGGACGC  
 TGCCCCCAGGGCTGGGTGTCCCTGGGCGGTGCGGACCTGAGGAAGAGCTGAGTCTCACCTTT  
 GCCTCTGAGACAGCAGAATGTGGAAGACTCTCGGAGCTGGTGACGGCTGTGTCCGGATCCGAC  
 CTCTCCTCAATACGGAATAACCTGACCCCTAGAGAATGTGGCTGATCTGGTGAGGGCCATCCC  
 CACTGACCCTCCACACGGTGCAAAAAATGGCTCTTGGCAGCCGGAGCCGAGAAGTGCCATTCT  
 GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
 TGGGGCTGAGTTTTCATCATATGTGGGAGGACCTACGGAACCCATGTTGTAAGGTCCCCAC  
 ATCCCTACCAGCTTCCACAGGCCCTTGGCCCCCATGTGGACTTTGTGGGGGAGCTGCACCGT  
 TTTCCCCAACATCATCCCTGAGGCAACGCTCTGAGCCCGAGGTGACAGGGACTGTAGGCCCT  
 GCATCTGGGGGTAACCCCTCTGTGATCCGTAAAGCGATACAACCTTGACCTCACAAGACGTGG  
 GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCTGGAGCAGTATTTCCATGAC  
 TCAGACCTGGCTCAGTTTCATCGCCCTCTTCGGTGCCAACCTTGCCATCAGGCATCAGTAGC  
 CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGATTGAGGCCAGTCTAGATGTGCAGT  
 ACCTGATGAGTGCTGGTGCCAACTCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
 GGACAGGAGCCCTTCTGTCAGTGGCTCATGTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
 GCATACGTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA  
 AACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCCCTGCTCTTCGCCCTCAGGTGACAGT  
 GGGGCCGGGTGTGGTCTGTCTCTGGAAGACACAGTTCCGCCCTACCTTCCCTGGCTCCAG  
 CCCTATGTACACCAGTGGGAGGCACATCCTTCAGGAACCTTTCCTCATCAAAATGAAA  
 TTGTTGACTATATCAGTGGTGGTGGCTTTCAGCAATGTGTTCCACGGCTTCATACCAGGAG  
 GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC  
 CAGTGGCCGTGCCCTACCCAGATGTGGTGCACCTTCTGATGGCTACTGGGTGGTCAGAACCA  
 GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCCTCTACTCCAGTGTGGGGGGATCCCTA  
 TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAG  
 GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGAACCCGTGGCTGCCATGAGTCTGTCT  
 TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGTCTGGCTGGGATCTGTAAACAGGC  
 TGGGGAACACCAACTTCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCCTTTCTATC  
 AGGAGAGATGGCTTTGCCCTGCCCTGAAGCTGGCAGTTTCAGTCCCTTATTCTGCCCTGTG  
 GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCGAAA  
 TGCTGTGAGCTTGACTTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
 CCTGCCCTAGATTCTCAATAAGATGCTGTAACCTAGCATTTTTGAAATGCCCTCTCCCTCCGC  
 ATCTCATCTTTCTCTTTCAATCAGGCTTTTCCAAAGGGTGTATACAGACTCTGTGCACCTA  
 TTTCACTTGATATTCACTCCCCAATTCAGTCCAAGGAGACCTCTACTGTCCAGCTTTACTCT  
 TTCTACCTGACATCCAGAAACAATGGCCCTCCAGTGCACTACTTCAATCTTTGGCTTTATG  
 GCCTTTCCATCATAGATTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACTTCTCTG  
 ACTACTCTTGCTCTCTCTCTCATCAATTTCTGCTTCTTCAAGCAATCTGACCACTCATGTC  
 TCCATTGTAGATTTTTGCTCTTCTCAGTTTACTCATTGTCCCTGGAAACAATCACTGACA  
 TCTACAACCAATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA  
 TGTAAAAAA

## FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGYLTLENVADLVRPSPLTLHTVQKWLAAAGAKCHSVITQDFLTCWL  
SIRQAELLPLGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP  
EPQVTGTGVLHLGVTPSVIRKRYNLTSQDVGSGTSNNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMASAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPSSSYFNASGRAYPDVAALSDGYWVVSNRVPIPVVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPTGWTGPTSQLC

### Signal sequence:

amino acids 1-16

### N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

### Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

### Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

### N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## FIGURE 95

GCCGCGCGCTCTCTCCCGCGCCCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC  
GGGTGCTCGGCGCGGAACAGTGTCTCGGCATGGCAGGGATTCACAGGGCTCCTCTTCTCTCTC  
TTCTTTCTGCTCTGTGCTGTGTGGCAAGTGAGCCCTTACAGTGCCCCCTGGAACCCACTGTG  
GCCTGCATACCGCCTCCCTGTGCTCTTGTCCCCAGTCTACCTCAATTTAGCCAAGCCAGACT  
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCAGTGTCATAAGGGAAC  
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC  
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC  
AGGTTCAGCATTTTTGGGAAGGACTTCTGTCTCAACTACCCTTTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAAGCATGTCTCACAGCTGCCCACTGCA  
TACACGATGGA AAAA CCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCTTAAAGCCC  
AAGTTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCGAGCAGATGAA  
ATTTTCAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAAC TAAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGCCAGAATTCACCTCTC  
TGTTTATGACAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCTCTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATATTATGGCATT TTTTCAGG  
GCACCAGTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTGAGAACTACTC  
CTCTCAAATATGCCCAGATTTGCTATTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG  
TGACACAGTGTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCC  
AAATTGTTTTTTGTCAATTGGCGTGACACGTTGTGTGTGTGTGTGTGTGTGAAGGTG  
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAAC TG  
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAA  
AAAAAATACTGATTTGGGGCAATGAGGAATAATTGACAATTAAGTTAATCTTCACGTTTTTG  
CAAAC TTTGATTTTTTATTTTCATCTGAAC TTTTCAAAGATTTATATTAAATTTTGGCATA  
CAAGAGATATGAAAAAAAAAAAAAAAA

## **FIGURE 96**

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAACHIDGKTYVKG  
TQKL RVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD  
AQP GASGSGVYRVMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNAVVRITPLKYAQICYW  
IKGNYLDREG

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 93-97, 207-211

### **Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

### **Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

### **N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

### **Serine proteases, trypsin family, histidine active site.**

amino acids 171-177



## FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGGCGGGCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC  
ACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCCTACCTGATGCCCTCTATCCACCT  
CCCTCCAAACACCCCATGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCCTCAGACCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA  
GCTCCGCGGGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG  
CCGCGCGCTCTTAGGCGCGAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCTCGGGCGGTTTCCCCCGCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC  
GGCCTCAGGCCCCCTTCCAAGGCATCAGGCCCGGCCAACGGCCTCATGTCCCCGCCCCAC  
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAAATGTTAATGATTTTAT  
AGGTATTTGTAACCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATTTATTTAT  
CTCAAAAAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFSTLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAACHCFKDNLNKPYLFSVLLGAWQLGNPGRSRSQKVGVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSESVLPICLPDASIHLPPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIDSEVCSHLYWRGAGQGPTEDMLCAGYLEGERDACLGDSGGPLMC  
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG  
SGAAARS

### **Signal sequence:**

amino acids 1-32

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCCACCAATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGTTGGCCACCAAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGGATGGT  
GGAGCTGCACAACTCTACCGGGCCAGGTATCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCCCTTCGCCAAGGCCACGACACGGCAGTGCGCTGTGGGGCCAC  
AACAAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCCGCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGATGGCACCAACGAGCGTGAGCACTACAACTCAGCGCCGCCACCT  
GCAGCCAGGCCAGATGTGCGGCCACTACACGAGGTGGTATGGGCCAAGACAGAGAGGATC  
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGGAACCGCCCTACCAGGAGGGGACTC  
CGTGTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCTTACCTGGTAACTGAGGCCCATCCTTCCGGGGCACTGA  
AGCATCAGACTCTAGGAAAAATGGGTACTCCTTCTCCCTAGCAACGGGGATTCCGGCTTTCT  
TGTTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAACCCAGGCC  
CCAATTCTTTAGCAACGAAAGACCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC  
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCAGAGAACTCTTGAGCCCAAGATGTCCCTGACAGGGGCAAG  
GGAATCTTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCTTCCAGTG  
AGGTCTTGGCCTCAGTTTTTCCAGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCCTGCCCAATTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA  
AGCCTAGCGTTGTGTGAGGCTGAACTCGGGCCCTGGTATGTGTGGGGCCCTCTCCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTTGAATGGGATACCACTCAAAGGG  
TGAAGAGTTCAGCTGTCTCCTGTCTCTTCCCCACCTGTCCCCAGCCCCCAAACAAGATA  
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAGGCTACGGGGCATGTGCCCTCATCACACCATCC  
ATCCTGGAGGCACAAGCCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC  
GGGCCACACCTCTCTGCCCTCCTCCTGAGTCTGGGGGTGGGAGGATTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGGCTGTCTGCCCACACAGCATGTGCGCTCTCCTGAGTGCCTG  
TGTAGCTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTT  
TTTGTAGTGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYRAQVSPTASDMLHMRWDEE  
LAAPAKAYARQCWVGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLGQVEETNIELLVCNYPEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFILVTEV  
SGSLATKALPAVETQAPTSLATKDPSPMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS  
THVIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGDPDKPSV  
SGLNSGPGHVWGPLLGLLLPLPLVLGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

# FIGURE 101

GTAAC TGAAGT CAGGCT TTT CAT TTG GGAAG CCCCT CCA CAGA ATT CGGT CAT TCT CCAAGT TAT **ATG** GTGGACGT  
 ACT TCT GTT GTT TCT CCT CTG CTT TCT TTT CAC ATT AGC AGC CGGACT TAA GT CACA ACAG ATTAT CTTT CAT  
 CAAGGCAAGT TCCAT GAGC CACCT TCAAAGCCCT CGAGAAGTGA AAC TGAACACA AATGAAT TGGAGACCA TCC  
 AAATCTGGGACCA GTCTGG CCAATATTACACTTCTCTCT TGGCTGGAA CACAGGAT TTTGAAATCTCCCTCA  
 ACA TCTGAAGAGT TTT CAGTCCCTTGA AACCTTTGGACCTTTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATT  
 TCCAGCCCTACAGCTCAAATATTCTGATCTCAA CAGCAACCGAGTCA CATCAATGGAACCTGGGTATT TTAGCAAA  
 TTTGGC CACA CACACTCTCTGTGTTTAAAGCTGAA CAGGAACCGAATCTCAGTATCCCA CCAAGATGTTTAAACT  
 GCCC CAACTGCAACATCTCGAATTTGA AACCGAAACAA GATTAAAAATGTAGATGGACTGACATTTCAAAGCCTTTGG  
 TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAA CCGAAACTTATGGATGGAGCTTTTTGGGGGCTGAGCAA  
 CATGGAAATTTTGCAGCTGGACCATAA CAACTCAACAGAGAT TACCAAAGGCTGGCTTTACGGCTTGCTGTGATCT  
 GCAGGAATCTTCA TCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCTGGGAGTCTCGCCAGAACTCTCAG  
 TGAGCTGGACCTAACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTCTGGCCTAAGCTTACTAAATAC  
 ACTGCACATTTGGGAACAACAGAGTCA GCTACATTGCTGATTGTGCTCTCCGGGGGCTTTCCAGTTTAAAGACTTT  
 GGATCTGAAGAACAA TGAATTTCTTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTTGAG  
 GCGACTGATCTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCAATTGGAGCA  
 TCTAGACCTGAGTGACAACCGCAATCATGCTCTTTACAAGGCAATGCATTTTCACAAATGAAGAAACTGCAACAAT  
 GCATTTAAATACATCAAGCCTTTTTGTGCGATTGCCAGCTAAATGGCTCCCA CAGTGGGTGGCGAAAACCAACT  
 TCAGAGCTTTGTAAATGCCAGTTGTGCGCCATCCTCAGCTGCTAAAGGAAGAAAGCACTTTTGCTGTTAGCCAGA  
 TGGCTTTGTGTGTGATGATTTTCCCAAACCCAGATCAGGGTTAGCAGAGAAACAGTCCGGCAATAAAGAGCTTC  
 CAATTTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGATTTCCCAATGACTTTTGCTTTGAAAAAAGACAATGA  
 ACTACTGCATGATGCTGAAATGGAAATATTAGCACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTATACCA  
 CATCTCTCGGCTCGCGAGGTGGAAATTTGCCAGTGAGGGGAAATATCAGTGTGCATCTCCAATCACTTTGGTTT  
 ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCAATGGATCTCACCAT  
 CCGAGCTGGGGCCATGCCAGCTTTGAGGTGTGCTGCTGTGGGGCACCAGCCCC CAGATAGCTGGCAGAAGGA  
 TGGGGC CACAGACTCC CAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGT  
 GGATGTGAAGATAGAGGACATTTGGGGTATACAGCTGCA CAGCTCAGAACAGT CAGGAAGTATTT CAGCAAATGC  
 AACTCTGACTGTCTAGAAAACCACTCAATTTTGGCGGCAC TGTGTGACCGAACTGTGAACCAAGGAGGAAAACAGC  
 GCTCTCA CAGTGCAATTTGTCGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATGATGCCATTTGGTGTG  
 AACCCAGAGGCACATTTTGGCAGGCAATCAGCTTCTGATTTATGTGGACTCAGATGTCAGTGTATCTGGGAA  
 ATACACATGTGAGATGTTCTAACCCCTTGGCACTGAGAGAGGAAACGTCGCCCTCAGTGTATCCCCACTCCAAC  
 CTGGCACTCTGCTCAGATGACAGCCCATCGTTAGACGATGACGATGGGCCACTTGGGTGTGCTGATCATAGC  
 CGTGGTTTGTCTGTGGTGGTGCACGTCATCTGCTGTGGTGGTCTATCATATACACAAGCCGAGGAGATGAAGA  
 TTGACATATTACCAACACAGATGAGACCAACTGTGCCAGCAGATATTCTGATTTATTGTCTCTCAGGGAACGPT  
 AGCTGACAGGCAGGATGGGTACGTGCTT CAGAAAGTGGAGCCACCAAGCTTTGTCA CATCTTCAAGTGTCTGG  
 ATTTTCTTACCAACAATGACAGTATGGGACCTTGCCATATTGCAATACAGTGAAGCTGTGAGTGGAGCTGC  
 CACAGATCTGTCTCTTTGTCTCGTTTTTGGGATCCACAGGCCATATGTGATTTGAAGGGAATGTGTATGTGCTCAGA  
 TCTCTTTTGAACATATCATACAGGTG CAGTCTTGACCCCAAGAACAGTTTAAATGGACCATATGAGCCCACTTA  
 CRTAAAGAAAAGGAGTGTCTACCCATGTTCTCATCTT CAGAAGAACTCTGCGAACCGGAGCTTCAGTAATATATC  
 GTGGCCTTCACATGTGAGGAAGCTACTTAACTAGTTACTCTCACAATGAAGGACCTTGAATGAAAAATCTGTG  
 TCTAAACAAGTCTTTTATGAGTTTATGTGCAAACTCAGAGCCAGGCTCGGTTGCCCTCGAGTAATTTCTTATGGG  
 TACCTTTGGAAGAGCTCTCAGGAGACCTCACCTAGATGCTATTTCAAGCTTTGGACCGCATCAGATTGATGTGAGCC  
 AAGAGCCTTTTATTTGAAGCTCATCTCTCC CAGACTTGGACTCTGGGT CAGAGGAAGATGGGAAGAAAGAGGAC  
 AGATTTCTCAGGAAGAAATCATTGTGTACCTTTAAACAGACTTTAGAAAACATCAGGACTCCAAATTTTTCAGT  
 TTTATGCTTTGGACAGATAGACTAGACTGAATGAGACCAAAGGAAAAGCTTAA CATACTACTCACTCAAGTAACTTTTATTTA  
 AAAGAGAGAGAACTTTATGTTTTTAAATGGAGTTATGAATTTTAAAGGATAAATATGCTTTATTTATACAGAT  
 GAACCAAAATACAAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAA TACCTTTTAAACTA  
 TTTTAACTTTGTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTTATTTATGTTATTT  
 TTATAAGTCAGATTTCTTTTTTATGGAAAATGAGTTACTAAAGCACTTTAAATAAATACCTGCCTTGACCACTTT  
 TTAATAGAAGTTACTTCATTATATTTCACATTTATATTAAATAAATGTGCAATTTGA

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## **FIGURE 102**

MVDVLLFLSLCLLFHISRDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSA  
ITLTLAGNRIVEILPEHLKEFQSLTDLSSNNISELQTAFFALQLKYLNLNSNRVTSMP  
GYFDNLANTLLVLKLNRRNRSAPKPMFKLPQLQHLELNRNKIKNVDDLTFQGLGALKSLKM  
QRNGVTKLMDGAFWGLSNMEILQLDHNNTLTKGWLYGLMLQELHLSQNAINRISPDWE  
FCQKLSLDDLTFNHLRSLDDSSFLGLSLLNTLHIGNRVSYIADCAFRGLSSLKTLDLKNN  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLFSICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAGG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFSSSYSVKAKLTVNMLPSFTTKTPMDLIRAGA  
MARLECAAVGHAPQIAWQKDGDTFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPKLNWTKDDSPLVVTER  
HFFAAGNQLLIIVDSVDAGKYTCEMSNTLTERGNVRLSVIPTPTCDSQPMTAPSLDDDG  
WATVGCVIIAVCCVVGTSLVVVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLD  
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSADVEAATDLFLCPFLGSTGP  
MYLKGNVYGSDFETHTGCPDPRTVLMHDHYPSYIKKKECYPCSHPSSECSERSFSNISW  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDPSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLDSGSEEDGKERTDFQENHICTFKQTLNRYRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

1000  
 900  
 800  
 700  
 600  
 500  
 400  
 300  
 200  
 100  
 0

AGGAGGAGAGATTTGACCATTAATAAGAGACTTTTTTTTGGTGTGTGGCTGTTTGGGTGCGCTTGCAAAAATAG  
 GCGGATGTCAGGACGCGACTTTCTCTCGGAACCGAAGCAATGGTAACTGATGTGCAAGAGAGAAAGGAC  
 GAAGCTTTTCTTGAGCCCTGGATCTTAAACAATATGTATATGTGCACAGGAGGACATTCAAGATGAAA  
 TAAAACAGAGTTAGACCCGCGGGGGTGTGTGTTCTGCATAATAATAATCTTAAAGCAGCTGTCCCTCC  
 CCACCCCCAAAAAAGGATGATTGAAAATAAGAACCGAGGATTTCAAAAAGAAAAGATTTGATTCTTTCTC  
 TATAAAGSAGGAAAGCTGAGCCAGAGGATATTTTGAATGAAAAGTTTGGGGCTTTTATGAAATGAAAGACT  
 GGTGTGTGTGGTCTTTCTTTCTTTTGAATTTCCCAACAAGAGAGAGAAATTAATATATCATCTGCAAAAZA  
 TTTCAGAGAGAAAAGTTGAACGCGCGGCAATGGAGCAATTGATTGGGGGAGAGAAAACAGCAGAGCACTTGCG  
 TTTGTGCTCATTTTGACTAAATGAGCGGATATTCAGTTGGATTTTCTTCATCAACCTCTTTTTTTAAAT  
 TTTATCTCTTTTGGATCAAGATCATTCGCTTTTCTCTGTCTTAAACCCTGGATTTCCATCTGGATGTGCTG  
 GTGATCAGCTTGAAATACAACTGTTGAATTCCAGAAGGACCAACAGATAAATATGGAATTTGAACAGAT  
 GACCTTCATATCCACAGCATATGATAGTGTCTAGTTTAAACGGGCCATATTTGACCCCGCTGTTGTGGTGTG  
 CTGGCTCTCTCAACTCTTGTGTGTGCTGTGTGCTGGCGCTCAGACTGCCCTCTCTGTGTGCTCTCGAGCAAC  
 CCAAGTTTCAGCAAGGTGATTTGTTGTGGAAGAAACCTCGTGGAGGTCGCGATGGCATCTCCACCAACACACCGCT  
 CTGAAACCTTCAGTGAACCAATACAGATCATCAAATGAGTCAAGCTTCAAGCATCTGGAGCTTTGAAATCTC  
 AACTTTGATGACAGCCATATCAGAACCAATGAAATGGGGCTCTCAATGGTCTGTGGCAACCTCAACATCTGGA  
 ACTCTTTGACCAATCGTCTTACTACATCCCAATGGAGCTTTGTATCTGTCTAAACTGAAGGAGCTCTGGTT  
 GGAAGAACCCCACTGAAGAGACTCCCTCTTATGCTTTTAAACAGATCTCTTTTGGCGCATAGACTTAGG  
 GGAATTTGAAAGACTTTTATACATCCAGAAGTGCTTTGAGGTCCTTCAAGTCTGCTCAACTGAGGATTTGAACCTGC  
 ATATGTCACACTCTCGGAAATCCCTTAACCTCACACCGCTCATAAACATAGATGTGCTGGATCTTCTCGGGAATCA  
 TTTATTCGCATCAGCGCTGGCTCTTTTCAGGGTTTGATCGACTTCAAAAGTTGAGTGATGATACCCAGAT  
 TCAAGTATGAAACGGAATGCCTTTGTCAACCTCTCAGTCACTAGTGGGATCAACCTTGGCACAATAAATCAAC  
 ATTACTGCTCATGACCTCTCACTCCCTGTCATCATTCAGAGGGATATCTTATCATCAACCCCTTGGAACTG  
 TAACTGTGACATATCTGTGCTCAGCTGGGTGGATTAAGAACATGTGGCCCCCTGCAACACAGCTGTGTTGTCGCGGT  
 TAAACCTCTCCCAATCTAAAGGGGGAGGTATATGGAGAGCTGCACAGAAATTACTTCATGATCATGCTCCGGT  
 GATTGTGGAGCCCCCTCGAGACTCTCAATGTCTCAAGGGCATGGAGCTGAGGCTGAAATGTGCGGCTCCCATCT  
 CTCGATCATCTGATTTGATTACTTCAAGTGAACCACTCATGACATCTGGGAGGCTCAAAAGTCCGGATAGCTGT  
 GCTCATAGATGGTACGTATAATTCTCACAATGTAACTGTGCAGATACAGGCATGATCATGATGTATGTGAGTAA  
 TTCGGTTGGGAATCTACTGCTTCCAGCCCACTGATTTGTACTGCAGCAACCTACTCTTTCTCTTACTTATCT  
 AACCGCTCAGTGAAGACTATGGAACGCTTCAGGATGAGGCACGGAACAGATACAATGTGGGTCCCACTC  
 AGTGGTGCAGTTGGGAGACCAACCATTTGTGACCACTCTCTCACACACAGAGACAAGGTGCAGACAGAAAACCTT  
 TACGATCCCGATGATGATATAAACAGTGGGATCCAGGAATGTATGAGGTCTATGAAGATCCAAAATATCATCT  
 TGGGTTTGTGTGGCCATCACACTCATGGCTCAGTGTGCTGTCTATTTCTACAAGTGAAGGAGACGAGCACTC  
 TCGGCAAAACCATCAGCCCCAACAGGACTTGTGAATTTAATATGGTATGAGATTACGGGAGACACACCC  
 CATTGAAAGGCCACTGCCATGCTGTCTATCGAGATGAGCACTAAATCACTATACTATACAAATCTCCCTT  
 CAACCAACCAACATGACATGATACAAATAAATCAATACAGTTTCAGTGTCAAGCGTTTATGATCCGAATGAA  
 CTTCAAGACAAATGTACAGAGACTCAAAAT**TAA**AAATTTACAGATTTCAAAAATAAAAACAAACAAATAAAAAA  
 GACAGTTTATTAATAATGACAATAAGTCTGGCTCAAAATCTATGTTTCAAAAAGTGTCTTTCAAAAATAACAA  
 AAAAAAGAAAATTTTATTATTAAAAATCTATGTGATCTAAAGACAAA

## **FIGURE 104**

MLNKM TLHPQQIMIGPRFNRALFDPLL VVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVDPDGISTNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNPNIESIPSYAPNRIPSLRRLDLGLKRLS  
YISEGAFEGLSNRLRYNLAMCNLREIPNLTPLIKLELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGT LNFTNVTVDGTGMYTCMVNSVGN  
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGTPVVDWETTNVTTSLTPQ  
STRSTEKFTTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRQHRQN  
HHAPTRTVEIINVDDEITGDTPMESHLMPAIEHEHLNHNYSYKSPFNHTTTVNTINSIHS  
VHEPLLIRMNSKDNVQETQI

### **Signal sequence:**

amino acids 1-44

### **Transmembrane domain:**

amino acids 523-543

### **N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

### **Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

### **N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537



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TGAAGGCGCTGCTCAAGCTCAAACTCTGTGTGCAATTTGAGCTTTGGAGTTCTTTTCGGTTTCCCTCCCTCTGTTTGGGGGGGGA  
 TGAAGGCGCTTCCCGCCGGGATTAAGAAGAAATTTAGCCGGGACGCGAGGAGGAGCGCGACGCGACGCC  
 GAGGCGGGCGGTGACCACTTCGCTCGGCTGGAAGATTTTGTCCGGGGCCCAAGCGCGCCGCGTGGGAGCTTTCGGGTAGA  
 GACCTTAGGCCCTGGACGCTGAGATGAGAGCGCGCGGAGCCCTCTGTCGGCGCGCGCGGGGTTGGGGTGCTGCTGTGCTGTC  
 GCGGTGTGGGGCGGCTGGCGGTTCGACAGCGCGGCTGTCCGGGGAGCAATCGGCGAGCCCTCTTGGGGTAGTGGCGC  
 GAGCGCCCATCGCCCACTACCTCTCGGCTGCTGCTGGGAGCTGCTGGAAGCTGAGCTGTAAAGCGGCTAGCGCTCTGCT  
 CCGGACGACCTCCGCTCTGGGTGCTGCGGTGCTGTAATGACACACAGATATTTCTCTCAAGGACAGTCTTC  
 ATGAGCGCACTTCCAAAGCTTTCGAGAAGGTGAACGAAACCAATGAATTTGGAGACACTTCCAAATCTGGGACCA  
 GTCTGGCGAAATTTACACTTCTCTCTGGGTGGAACAGGATTTGTGAAATCTCCCTGAACTCTGAAGAG  
 TTTCACTGCCCTTGAACCTTTGGAACCTTAGCAGACAAATATTTCCAGAGCTCCAAATGTGCAATTTCAAGCCCTACAG  
 CTCAAATATCTGTATCTCAACAGCAACCCAGTACCAATGAAACCTGGGTATTTGCAATTTGGCCAAACACAC  
 CTCCTTTGTTTAAAGCTGAAACAGGAACCGAATCTCAGCTATCCCAACCAAGATGTTTAAACGCGCCCAACGTCAA  
 ATCTCGAATTTGAACCGAAACAGCAATTAATAATGTATGATGAGCTGACATTTCAAGGCGCTTTGGTGTCTGTGAGTCT  
 CTGAAATCTGCAAGAAATGGATGTACGAATATTTAGATGAGCTTTTGTGGGGCGTAGCAACATGGAAATTTTG  
 CAGCTGGACCACTAAACCACTAACACAGAGATTACCAAGAGTGAGCTTTTACGCGTGTGATGCTGCGAGCAATTCAT  
 CTCAGCCAGAGATCGCATCAACAGGATCAGCCCTGATGCTCGGGATGTTTGGCAGACAGCTCAGTAGCTGGACATCT  
 ACTTTCAATCACTTATCAGGTTAGATGATTTCAAGCTTCTTGGCTTAAGCTTACATAATAGCTGCATCTGGG  
 AACCAAGAGATCGAGCTACATTTGCTGATTTGCTCTCCGGGGGCTTCCAGTTTAAAGACTTTGGATCTGAAGAAC  
 ATAGAAATTTCTGGACTTGAAGCAACATAAATGGTGTCTTCTGGGCTTGACAACTAGGCGACGACTGATCT  
 CAAGGAAATCGGATCGCTTTATTAATATAAAAGCTTCACTGTGTTGATGATGATGGAGCATCTAGACGCTAGT  
 GCGAGACCAATCATGTCTTTTCAAGGCAATGCATTTTCAAAATGAAGAACTGCAACATTTGCATTTTAATACA  
 TCAAGCACTTTTGTGCGATTTGAGCTTAAATGGCTTCCGACAGTGGTGGCGGAAACCACTTTGACAGCTTTGTA  
 ATAGCACTTTTGCCCACTCCAGCTGCTAAATGGGAGGAAGCAATTTTGTGTTATAGCCCAATGCTTTGTGTGT  
 GATGATTTTCCAAACCCAGATCAGCGTTGACCCAGAAACAGCTGCGCAATAAAGGTTTCAACTTTGAGTTTC  
 ATCTGCTCAGCTGCGACGACGATGATTTCCCAATGACTTTTGTCTGAAGAAGACATGTAACCTACATGAT  
 GCTGAAGTGAAGAAATTAGCACTCCGGGCGCAAGTGGGAGATGATGAGATGATACCAACCTACTTCCGCTGT  
 CGAAGGTGGAATTTGCGATGAGGGAATATCAGTGTGCTTCCATCACTTTGGTTCTACTCTCTCTGCT  
 AAAGCCAGCTTACAGTAATATGCTTCCCTCATCCACCAAGCCCCAGATCTACACTCCGAGCTGGGGC  
 ATGCGCACTTGGAGTGTCTGCTTGGGACCCAGCCCCAGATAGCTGTGCGCAAGGATGGGGGCGACAGAC  
 TTTCCAGCTGCGACGGGAGAGCGCATGATGTGATGCCCGGAGTAGCGTTTCTTATCGTGGATGTAAGATA  
 GAGGACATTTGGGTATACAGCTGCTCAGCTCAGACAGCTGAGCAAGATTTTCAGCAAACTGCAACTGATCTGTC  
 CTGAAGAACACATCATTTTTCGGGCACTTGTGGACGAACTTAACGAGGGAGAAAGCGCGTCTCATAGTGG  
 ATTGCTGGAAGAGGAGCTCCCTTAACTGCACTGCACTGACCAAGAGATAGGACCTTTGGGGTAAACCGAGAGGAC  
 TTTTTTGCAGCGCAATCAGCTTCTGATTTTGTGGAATCAGATGTCAGTGATGTGGGAGTTACAGCTGTAG  
 ATGTTCAACCGCTTGGCATGAGAGAGGAAACGTGGCGCTCAGTGTGATCTCCCACTCCAACTCGCACTCCCT  
 CAGATGACGAGCCCTCATCTGTAGACAGTAGCAGTGGGCACTTGGGGTGTGTGATCATACCGTGGTTTGTGTT  
 GTGGTGGGCACTGATCTGCTGTGGTGTGCATCATATACACACAGGCGGAGGAATGAAGATTCGCACTATCC  
 AACAGAGATGAGCAACTTGC CAGCAGATATTTCTAGTTATTTGTCATCTCAGGGAAGCTTAGTGTGACAGG  
 GATGGGTAGCTGTCTCTCAAGAAATGGAGGCCAACCAAGTTTGTCACTCTTCAGGTGTGGGATTTTCTTCA  
 CAGATACGACGTAGTGGGACTGCTCATTTGCAATATGCAATGAGTGAAGCTGATGTGGAGCTGCGACAGATCTGTT  
 TCTTGTGCGTTTGGGATCGACCGGCCCTAGTTTGAATGGGAAATGTGATGTAGCTCAGATCTTTTGAACA  
 CATTCATACAGTTGCGATCTTGACCGAGAAACGATTTTAATGAGCACTATGAGCCGAGTACATAAGAAGAAAG  
 GAGTGTCTACCAGTTCTCATCTTTCAGAAGAACTCTGCGCAAGCGGCTTGAGTAATATCTGTGGGCTCTCAT  
 GTGAGGAGCTACTTAACTAGTACTTCTCACTAATGAAGCACTGGAATGAAATTTCTGTGTCTAAACAGCTGT  
 TCTTTAGATTTTGTGCAAGATCCAGAGCGAGCTCGGTTGCTTCAGTAATTTCTTCACTGGGTACTTTGGAAGA  
 GCTCTCAGGAGACTCAGATAGTGCTATTTCAAGCTTTGGAACACTCAGATTTGACGCGAAGAGCTTTTAT  
 TGAAGACTCATTTCTCCCGAGCTTGAAGCTTGGGTGAGGAGGAATGGGAAGAAGAGACAGATTTTCAGGA  
 GAAATTCACATTTGTACTTTTAAACAGACTTTAGAAGATACAGGACTCCAAATTTTCTGCTTTATGCTTGGAC  
 CATATGAGCTGATGAGACCAAGGAAAGTAACTTAACTACTACTCAGTGAAGTACTTTTAAAGAGGAGAGAT  
 CTATGTGTTTTTAAATGGAGTTGATGAATTTTAAAGGATAAAATGCTTTATATACAGATGAACCAAAATAC  
 AAAAGGATGTAAAAATTTTATACCTGGGAATGATGCTCATATAAGATACCTTTTAAACATTTTAACTTTG  
 TTTTATGCAAAAAGTATCTACGTAAATTAATGATATAAATCATGATTTTATGTATTTTATAATGCGGAG  
 TTTCTTTTATGAAATGAGTATATAAAGACTTTTAAATAATCTCGCTGTGACCAATTTTAAATGAGAGT  
 ACTTCATTTATTTTGCATATATTTTATAAAATGTGTCAATTTGAAAAAAGAAAAAAGAAAAAAGAAAT

## FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGFPVSANIT  
LLSLAGNRIIVEILPEHLKEFQSLLETLDLSSNNISELQTAFPPALQLKYLILNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRISAIIPKMFKLPLQLHLELNRRNKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMEILQLDHNHNLTEITKGWLYGLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFNHLRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSLKTLDLKNEIS  
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQHLNLTSSLLCQLKWLPLQWVAENNFOQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDE  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLLRAQGGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFSSSYSVKAKLTVNMLPSFTKTTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF  
FAAGNQLLIIVDSVDSDAGKYTCMSNTLTGERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA  
TVGVVIIAVVCCVVGTSVLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTADLRQ  
DGYVSSSESGSHHGFVTSSGAGFPLQHDSSGTCHIDNSSADVEAATDLFLCPLFGSTGPMY  
LKGNVYGSDPFETHTGCSPPDPTVLMDHYEPSYIKKKECYPSCSHPSEESCERSFSNLSWPS  
HVRKLLNTSYSHNEGPKMKNLCLNKSSLDPSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAGHSSPDLDSGSEEDGKERTDFQENHICTFKQTLNRYRTPNFQSYDLDT

### Signal sequence:

amino acids 1-27

### Transmembrane domain:

amino acids 808-828

### N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

### Glycosaminoglycan attachment site.

amino acids 886-890

### Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

### Tyrosine kinase phosphorylation site.

amino acids 667-675

### N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

### Leucine zipper pattern.

amino acids 58-80, 65-87

# FIGURE 107

CAAAACTTGCCTGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC  
 TGGGGGAGCGCTTGGCTGTGGGCGCGCTCGGCGCCGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
 CTGCTTCACAGAGCGCCTACTGGTGTAAACGGGAGAGGCCCTGGGTGGTCCCGTCCCCTATCCCTCCTTTATATA  
 GAAACCTTCCACACTGGGAAGGCGAGCGCGAGGAGGAGGGCTCATGGTGAAGCAAGGAGCGGCTGATCTGCAG  
 GCGCACAGCATTCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGAGCAACAGCTTGCCTGGT  
 TCCATCAGCCCTGGCGCCAGCGCATCTGACTCGGCACCCCTCGCAGGCACCATGGCCAGAGCCCGGTGCTGC  
 TGCTCTGCTGCTGCTGCTGCGCCACAGCTGCACCTGGGACTGTGCTTCCCGTGAGGGCCCCAGGATTTGGCCGAA  
 GTGGCGGCCACAGCCTGAGCCCGGAAGAGAAGCAATTTGCGGAGAGGAGCGCGGTGCTGGTACTGAGCCCTGAGG  
 AGCCCGGGCTTGGCCAGCGCGGTGAGCTGAGCCCGGAGACTGTGCTGTTCAGGAGGGCGTGTGGAGCTGTG  
 GGGTATTGACTTGGCTGAGTTCCCGGGGCTGCTGCTGAGCACAACCAACCTATCTCTGCAGAAACAGCAGC  
 TGGAAAGATCTAACCCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACAGCCGCTGA  
 CTTCGCCGAGGGCTCCAGAGAAAGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAAATAACAGC  
 TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGAGCTTTGCTGCCAACTATCTCACCAGATCT  
 ATGGGCTCACCTTTGGCCAGAAAGCCAACTTGAGGCTCTGTGTAACCTGCACAACAAGAGCTGGCAGACGCGGGC  
 TGCCGGACAACATGTTCAACGGCTCAGCAACGTCGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC  
 CCAAGCAGCTGCGCGCTGCCCTGTAACAGCTGCACTCAAGAACAACAAGCTGGAGAGATCCCCCGGGGGCT  
 TCAGCGAGCTGAGCAGCTGCGCGAGCTATACCTGCAGAACCACTACCTGACTGACGAGGGCTGGACAACAGAGA  
 CCTTCTGGAAGCTCTCAGCGCTGGAGTACCTGGATCTGTGCAGCAACAACCTGTCTCGGGTCCAGCTGGGCTGC  
 CGCGCAGCCTGGTGTGCTGCACTTGGAGAAGAACGCCATCCGAGAGGTGGACGCGAATGTGCTGACCCCATCC  
 GCAGCCTGGAGTACTGTGCTGTCACAGCAACCAAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC  
 TCAAGCGGTGTCACACGGTGCACCTGTACAAACAACGCGCTGGAGCGGTGCCAGTGGCCTGCCTGCGCGGTGC  
 GCACCTCATGATCTGCAACAACAGATCAGGGCATTTGGCGCGAAGACTTTGCACCACTACTTCTTGGAGG  
 AGCTCAACCTCAGCTACAAACGATCACAGGCCACAGGTGCACCGGAGCGCTTCCGCAAGCTGCGCTGCTGC  
 GCTGCTGGACCTGTGCGGCAACCGGCTGCACAGCTGCCACCTGGGCTGCCATGAAATGTCCATGTGCTGAAGG  
 TCAAGCGCAATGAGCTGGCTGCTTGGCACGAGGGGCGTGGCGGGCATGGCTCAGCTGGGTGAGCTGTACCTCA  
 CCAGCAACCGACTGCGCAGCGAGCCCTGGCGGGCGTGGCTGGTGGACTTCCGCCATCTGAGCTGTGGACA  
 TCGCGGGAATCAGCTCAGAGATCCCCGAGGGGCTTCCCGAGTCACTTGAGTACCTGTGACATGAAGCAACA  
 AGATTAGTGGCGTCCGCGCCCAATGCTTCGACTCCAGGCCCAACCTCAAGGGGACTCTTTTCAGGTTTAAACAAG  
 TGGCTGTGGCTGCTGCTGGACAGTCTTCCGAGGGCTGAAGCACTGAGCTTGGACATTTGAAGGCAACCT  
 TAGAGTTTGTGATTTTCAAGGACCGTGGCGCTTGGGGAAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 AGGAAGAGGAACAAGATAGTGACAAAGGTGATGCAGATGTGACTAGATGATGACCCCGGACTCTTTTCTGC  
 AGCACAACCTGTGTGCTGTGAGCCCCACTTGGCTGTCTACACAGCAACCAAGCTGCACATATGAGGCA  
 TCCCACTGCGCTGACAGTGTGATGCTGATGATACACACCAACACATGCAACAGCTGATGTGCGAA  
 CAGCCCTCCAAAGCCTATGCCACAGACGCTTTGCGCCAGCAGAATCAGCCATAGCAGCTGCGCGTCTGCCCT  
 GTCCATCTGTCCGTCCGTTCCCTGGAGAAGACACAAGGGTATCATGCTCTGTGGCCAGGTGCGTGCACACCTCT  
 GGAATCACAAGAGCTGGCTTTATTCTCTTCCATCTATGGGAGCAGGAGCCTTCCAGACTGTGCGCTGGCC  
 TGGCCCAACCTGCTCTCCAGGTGCTGGGCGATCACTGTCTAAGAGTCCCTTCCGCAACGCCCTGGCAGGACA  
 CAGGCACTTTTCCAATGGGCAAGCCAGTGGAGGAGGAGTGGAGAGGCCCTGGGTGCTGCTGGGGCTTTGGG  
 CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 GTTCTTCAGGCGTTGGGGGAGATCCGGGTGCCTTTATTTTATTTTATTTTCTTAAGGAAAAAATGATAAAAAAT  
 CTCAAAGCTGATTTTCTTTGTAAGAAATCAATATAAAGCATATCCCTATCCCTGCACAAAAA

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## **FIGURE 108**

MEGEEAEQPAWFHQPWPRGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPENEFPAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLF  
EHTNHLSSLQNNQLEKIYPEELSRHLRLETLNLQNNRLTSRGLPEKA FEHLTNLNYLYLANNK  
LTLAPRFLPNALISVDFAAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFMGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSRLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSV DANVLTPIRSLEYLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSCGNRLHTLPPGLPRNVHVLKVKRNELAAAL  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISK  
RGRLGKEKEEEEEEEEEEEETR

### **Signal sequence:**

amino acids 1-48

### **N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

### **N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

### **Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

**906-870-0000**

CAGGAGGGGCTCTCGGGGCGCGGCGACAGCAGACTCTCTCGCGCGCGCGGCTCTCGCGCTGTCTCCGGGCGAGGGGACG  
 CAGTACGCGCGCGGCGGAGGCTCTGGGGTTCCTTCGAGACTCTCAGAGGAGGGCGGCTCTCCCATCGCGCGCCACACCC  
 CAACCTGTGTTCTTCGCGCGCCACTGCGCGCTCGCGCCCGAGGACCGCTGCCCAACATGGATTTCCTCTGGCGCTGGT  
 CTGGTATACCTTGTCTCTATCTCTACGCGCGCGCGCCGAGATCTGAGCGGGAGGTGGCCCGAGGCAAAATAGTGTCTCATGT  
 TGGCCTATGTGTTATGTGTGGGAGGATGTAGCTGTCTGTGGTGGTCTGGGCTCGCGAGTCTGGGGACAGTGTGCAGCC  
 TGTGTGCCAACCCAGATCGAAACATGTGTGAATGTATGTGCGCGCAACAACTGCAGGTGTCTATCTGGTATGTCTGG  
 AAAAACCTGTAAATCAAGATCTAAATGTGTGTGGCTGTGAAGCGCGCGCTGTGAAGCAAGGTGCATGAACACTCT  
 CGCGACAGTCAAGGTGCTATCTGTCTCAACCGATATATGCTCATGCGCGAGGTGTCTCTCGTCAAGTGCCTTGTACTCT  
 TCTCATGTGCAAACTGTCAATGTGCTGTATGTGTGTAAAGCAAAATACGCTGCGAGTGGCCATCCGCTGGCTGGCT  
 GCACCTGCTCTGTGTGGGAGGACTGTGTAGATGTGTATGATGTGTATGCTACAGGAAGAGCTCTTGCCCTAGATTT  
 TGGCAAGTGTGTCAACCTTTTGGGAGCTCATCTGCGAGTGTATGCTACATAAGGCTCTCGATCTCATGTGTGTGGAG  
 CAAATATCAATGTCTAGCATGACATGACGAGTGCATCTGTGTCAAGTGTATGCTGACGAGCAAGCTTTGCTCGATGTATTA  
 CGTACGTGGGTCTCAAGATGACGTCAAAATGTAAAGAAGGATACAGGAGTGTATGCTGACTGTGTGTATATCCCAA  
 AGTTATGATGTGAACCTTCAGGTGCAAAATCATGTACCCAAAGGGAATGTTCACATTTAAAGGGTGACACAGGAA  
 TAATTAATGTGATTTCTGTATGTGGAAGTCTTGTGTGGCTCGGAAGACCAATATTTCTCTCTCATCTATTCACAA  
 CAGGCGCTACTCTGTAAAGCAACAAACAGAGACTACACCAACCCGAAACCAACCAATTTCTATCTCACCACACCCACCA  
 CTGCCACACAGAGCTCAGAACACCTCTACACCTACACACCCGAAAGGCCAACACCCGGACTGACAACTATAGC  
 ACACGCTCGCATGTACCTCTCAGGAGGGATTCAGTGTGACACAGGCTACACAGACGCTCTCAAGAACCCAGAGG  
 AGATGTGTCTACGTCTTCTGTGATGCTGTAAATTTTGACATGGATTTGTGGATGGTACAGGAAGAACAACTA  
 TGATCTGCACTGGGAACCAATCAGGACCGACAGGCTGGACATATCTACAGTCTCGCGAGCCAAAGCCCACT  
 GGGAAAGACTGCACGCTTGGTGTACTCTTCGCGCGCTCATCATGATCTCAGGAGGACTGTGCTGTCTCATCTCAGCA  
 CAGAGTAATCGSGCTGCATCTGTGCGACACTCCAGCTGTGTTGTGAGAAAACACGCTGGCCACCGGACGCGCTGTG  
 GGAAGAAAGATGTGCCATGTCTGCGGACCAACAGATCATCTTGGCGGGGCTGTGATCATCAGAGCGAATACCA  
 AAGATGAATAAGGGTTGAAAAAAAGATCTATGTAGAAAATTTAAAGAACTGGGAATTTAGACTTTAGAGTGAAG  
 AGAAGACTGAGGGGCAACCAATGTGATTTTTCAGTATATGAAGGTTGGCACAGAGAGGTTGGGACACAGCTGT  
 TTCCTCATTTGCACTAAGAAATAGAACAGGAAGAACTGGCTTAGCATAGAGTATAAGGAGACTTTCTTGCAGG  
 GCGCCATTTGTAGAAATCTCATAAAAAAGAGTGTGAAAAATCTCAGTATCTCTCTCTCTCTTAAAAAATTAGA  
 TAAAAATTTGTCTATTTAAGATGTTTAAAGTGTCTTACCCAAAGAAAGTACAAATATAGAATTTCCCAA  
 AGATGTTTGTATCTCATAGTAGTATGAGCGTGAATAATCTTTAGAACATAATTAATTTGGAACAAGCTCTAATTTAGG  
 CATTTTCCCTCTTGACCTCTAATGGAGGGGTGTGAAGAGGGAAGCGGCCAAATGTGAGCTCTCATGAAATAT  
 TCTCTCCCTTATGGCAATCTAGCAATTAAGAAAAAAGAAACATATTTATCCAAATGAGAGTATGATGGAC  
 AGATATTTTAGTATCTCAGTAATGTCTTAGTGTGCGCGTGGTTTTCAGTGTCTCTCATGTGAAGGATATAGCC  
 TTTCACTTTGTCAATGCATGTGTTTCAGATTTTTTTTTTTAAAGAACTCTCAAGGAACACAGTCTCAGAGAG  
 ATTTTCACTCGGTTGCATTTCTCTGTCTGTGTGTGCAAGTATCTTGGCTGCTTGAGAAAGAGTGGCCCTGCCCC  
 ACACCGGCAAGTATTTTCTCTCACTCATCAGTATAGATTCAGTTTCTCTTATCATTGGACTCTCCAGGTTGCCAC  
 AGAACAGTAATATTTTTGAACAATAGGTACAAATAGAGGTTCTCTGTCAATTAACTGTGAAGAAAGCGAGGCTGG  
 AGGGGGAAAAATAATCACTTAAGCCTTTTGAGTAAAGGCAAGATATGCTGCTGATAGCTCCATTTTAAATGGTTTACT  
 TCTTTATGGTCAATAACCTGCGACAGCTGAGATGAAGGAGGAAAAATAATGAAATTTTACTTTTCGATGCCAA  
 TGATACATTTGCATAAATGCTGGAAGAGGTTTCAAAGTACTGTATACATCTGTTTATTTATTTATTTATGTTAT  
 CTAAATAAAAAATGTAGTGTGTTTTCAAATGGCTCAATAAAAACAATTAATTAATAAAAAACATTAATGTATTA

## **FIGURE 110**

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGEICIPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCCQYGCDDVVKGQIRCCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDLMIYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPGKNGTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTTPERTTGLTTIAPAASTPPGGITVDN  
RVQTDPOKPRGDVFSVLVHSCNFDHGLCGWIREKDNLDLHWEPIRDPAGGQYLTVSAAKAPGG  
KAARLVLPGLRMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 273-277

### **Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

### **Tyrosine kinase phosphorylation site.**

amino acids 199-206

### **N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

### **Cell attachment sequence.**

amino acids 382-385

### **EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTGCCCCCTTAGATTGTGA  
**AATG**TGGCTCAAGGTCTTCACAACCTTTCCCTTTCCCTTGGCAACAGGTGCTTGCTCGGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTTACCTTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA  
CACAAATGCCAAATACTTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGAATAACC  
AACACAAGTTCACCATGATGCCACCCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTCT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAATGGAACCTCTATCTGCCAGTCA  
GAAGATACAAGTCACGGTTGATGATCCTGTCCAAAGCCAGTGGTGAGATTCACTCTCTCCCT  
CTGGGCTGTGGAGTATGTGGGGAACATGACCCGTGACATGCCATGTGGAAGGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGGTGAGGAACCTGTGAGTAAATGGAAAGTGATATCATATGCCCATCATATATTAT  
GGACCTTATGGACTTCAAGTGAATTCGTATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT  
TGACCTTGGAGAGGCCATCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCGCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCCAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATTTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
CACAGAAGGAAAAATCATTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTGATT  
ATATCCATGTGTCTTCTTCTTCCATGGAAAAAATATCAACCCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATAAGGAAAGCTCAAAACATTTTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTCAGG  
ATTTCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTGTCACAGTACAGT  
GTATGAAGTTATTCAGCACATCCTGCCAGCAGCAAGACCATCCAGAG**TGA**ACTTTTCATGG  
GCTAAACAGTACATTCGAGTGAAATTCGAAGAAACATTTTAAGGAAAAACAGTGGAAAAAGT  
ATATTAATCTGGAATCAGTGAAGAAACAGGACCAACACCTCTTACTCATTATTCCTTTACA  
TGCAGAAATAGAGGCATTTATGCAAATGAACTGCAGGTTTTTCAGCATATACAAATGTCTT  
GTGCAACAGAAAAACATGTTGGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGTGTGACGG  
GGAGAACGAAAGTGACAGGGGTTTCTCATAGTTTTGTATGAAATATCTCTCAAAACCTCA  
ATTAGTCTCATCTCACACTTTCATATCATCAACATGAGACTATCCCTGTCTCACCTACAA  
TGTGGAACCTTACATTGTTGATTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG  
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTGTTATTGTTACAA  
CAAAGTAATAAGGATGTTGTACAAAAACAAAACATATGCCTTCTCTTTTTTTTCAATCACC  
AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAAGTACATTAAAGTCTATTTTTTA  
TTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTTCTGTTTTTGTCTTTTAAAAAAAAAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSSVNSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPGYGLQVNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 341-359

### **N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

### **Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

### **Tyrosine kinase phosphorylation site.**

amino acids 272-280

### **N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



GCAAGCGCGGAAATGCGCCCTCCGGAGTCTGCGATTCCCTTGGCAGTCTCTGGTGCTGTT  
GCTTTGGGGTGCTCTTGCGAGCCAGCGGGCGGAGCAACGTTTCGCCGTATCATCGGACGGAGA  
ACTCGGAGAACTCCCTGGAAGAGACTGGATGATAGAATTTATGCCCGCTGGTGGCCCTGCT  
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTGCTGAATGGGGAAGATCTCTAGGTTTAA  
TATTCGAAAGTAGATGTCACAGCAGCCAGGACTGAGTGACGGTTTATCATATCTGCTC  
TCTCATCTATTATTCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG  
AAGGACTCATATAAATCTTTATAAGTGATAAAGAGTGGAAGAGTATGAGCCCGTTTCATCAT  
GTTTGGTCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA  
TCAGGACGCTGCATAAATCACTTTATTGAAGACCTTTGGATTGCCAGTGTGGGGATCATATACT  
GTTTTTGCTTTAGCAACTCTGTTTTCGGGACTGTTATTAGGACTCTGTATGATATTTTGGC  
AGATTGCTCTTTGCTCTCAAAAAGGCGAGACACGACCATACCATACCTCTCAAAAAAT  
TATTTACAGAACTGCGACAACCTTTGAAAAAAGTGGAAGAGGACAAGAGCGGATGAAGAA  
GATGTTTCAGAAGAAGAGCTGAAAGTAAAGAAAGCAACAAAGACTTCCACAGAATGC  
CATAAGACAACGCTCTCTGGGTCCATCAATTGGCCACAGATAAATCCTAGTTTAAATTTTATAG  
TTATCTTAATATTATGATTTTGATAAAAAACAGAAGATTGATCATCTTTGTTGGTTTGAAGTG  
AAGCTGTGACTTTTTTGAAATTTGCGAGGTTTCAGTCTAGATTGCTATTAATTTGAAGAGCTCA  
CATTGAGAACAATAAAGCACTAGGTATACAAAGTTTGAAATATGATTTAAGCACAGTATGATG  
GTTTAAATAGTCTCTCTAAATTTTGAAAAATCGTGCCCAAGCAATAAGATTTATGATATTTGT  
TTAATAATAACCTATTTTCAAGTCGAGTTTGTAAATTTTACATTTCCCAAGTATGCTATTG  
TAGGATTAATTAAGAAGATATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTCTCTG  
TTTCACTGTGTGAAAAAAGAAAGATATTTCCCAATAAATGGGAAGTTTGCCCATGTGCTCAAG  
AAATGTGTATTTTCAGTGACAATTTCTGTGGTCTTTTAGAGGTATATTTCCAAATTTCTTGT  
ATTTTTAGGTTATGCAACTAATAAAAACTGATCTTACATTAATTAATTCAGTTTCTACACA  
TGTTAATACAGGATATGCTACTGATTTTAGAAGTTTAAAGTTACATGGTATCTCTTGATTC  
GACAAAGATTGATTTTCTCTGTATTTTCTTACTACTAGGGTACATTTTATTTT  
CAAAATGGATGATAATTTCTTGGAAACATTTTGTATGTTTGTAGTAACAGTATTTTGT  
GTTTCAAAGTGAAGTTTACTGAGAGATCCATCAAATTTGAACAATCTGTTGTAATTTAAAT  
TTGGCCATCTTTTCAGATTTTACATCATCTTCTGCTGAATCTCAACTTGAAATGTTTTTT  
TTTCTTTTGGATGTGAAGGTGAACATCTCGATTTTGTGCTGATGAAAGAGCTTGTA  
TTTTATCTTTTGAATTTGAAATTCAGAAAGCTTAATATAAAGGTTGCATCTACTCAGGAAAGA  
GCTTCTCTGTATGATGCTTAAATGATTTTGTGCTCATATACAGAAAGTCTTAAATGAT  
TTTACAGTCTGTAATGCTTGATGTTTAAAAATAAACATTTTATATTTTTTAAAAAGCAA  
ACTTCATATATTTCTGTGTTCTTCTGACTGTTAATTTAGGTGTGGGATTTACAGGTAAGA  
GCTAGTAGATGAACATTTTAGTGATTTTACTCTTTAAGAGAGCTAGAATACATAGTTT  
CACCTTAAAGAGAGGGGGAAATCATAAATACATGATCACTGACCATTACGTAGTAGAC  
AATTTCTGAATGTCCCTCTCTTCTAGGCTCTGTTGCTGTGAATCCATTAGATTACAGT  
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTTGACCAT  
AAAGAGTTTGGATGTGAATCTGTGATGCTTAGAAAAATCTCTAAGCACAAATAAACCT  
TTCTAACCACTTCATTAAAGCTGAAAAAATAAAAAA

## **FIGURE 114**

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIQRSLGPSLATDKS

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 182-201

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

### **Tyrosine kinase phosphorylation site.**

amino acids 107-115

### **N-myristoylation site.**

amino acids 20-26, 192-198

### **Amidation site.**

amino acids 25-29



## **FIGURE 116**

MKLWVSALLMAWFGVLSQVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAPVFNAYKLVKRLNTDWPALDVLVQDSAAAGFIANLSVQORQFFP  
TDEDEIGAALKMRLQDITYRLDPGTISRGEPLGTYQAMLSVDDCFGMGRSAYNEGDIYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR  
YFEQLLEBEREXTLTNQTEAELATPEGIYERPDVYLPERDVYESLCRGEVVKLTPRQKRLR  
CRYHHGNRAPQLLIAPFKEEDEDWSPHIVRYDVMSEDEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDPVVARVNRMRQHITGLTVKTAELLQVANYGVGGQYEPHFDPS  
RRPFDGSLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFRLPCGSTVEVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,

346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

# FIGURE 117

GCAGTATTGAGTTTACTTCCTCCTCTTTTGTAGTGAAGACAGACCATAATCCAGTGTGAGTGAATTTGATTGT  
TTCATTATTACCGTTTGGCTGGGGGTAGTTCGACACCTTACAGTTTGAAGAGCAGGCAGAGGAGTTGTGA  
AGACAGGACAATCTCTTGGGGATGCTGGTCTCGAAGCCAGCGGGCTTGGCTCTGTCTTTGGCCCTCATTGACC  
CAGGTTCTCTGTCTTAAACTGAAAGCCTACTACTGCTCTGTGCCCATCAATCCATTGATCTTGAAGGCTGTGCC  
CCTGGGGCACCACCTGGCAGGGGCTACCACCAGTGGAGCTGAGCTCCTCTGTTGGCTCTGCTCGCGCCAGCGCTTC  
CCTCTCATCTTAGGGCTGTCTCTGGGGTGCAGCCTGAGCCTCCTGCGGGTTTCTCGGATCCAGGGGGAGGGAGAAG  
ATCCCTGTGTCGAGGCTGTAGGGGAGCGAGGGGGCCACAGAAATCCAGATTTCGAGAGCTCGGCTAGACCAGAGTG  
ATGAAGACTTCAAAACCCCGGATTGTCCCTACTACAGGGACCCCAACAGCCCTACAAGAAGGTGCTCAGGAATC  
GGTACATCAGACAGAGCTGGGCTCCCGTGAGCGGTGTCTGGTGGCTGTCTGACCTCCCGAGCTACACTGTCCA  
CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCTCGGTACTCTACTTCACTGGGCGAGCGGGGG  
CCCGGGCTCCAGCAGGGATGCAAGTGGTGTCTCATGGGGATGAGCGGCCCGCTGGCTCATGTCAAGAGCCCTGC  
GCCACCTTCAACACACTTTGGGGCCGACTACGATCGGTTCTTCATCATGCAAGATGACACATATGTGACAGCCC  
CCCGCTGGCAGCCCTGTCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCCGGCAGAGGAGTTCAATTG  
GCGCAGGCGAGCAGGCCCCGTAATGTCTATGGGGGCTTGGCTACCTGTGTACGGAGTCTCCTGCTCTGCTCTGC  
GGCCACATCTGGATGGCTGCCGAGGAGACATTCCTAGTGCCGCTCCTGACGAGTGGCTTGGACGCTGCCTCATTG  
ACTCTCTGGCGCTCGGCTGTGTCTCAGACACAGGGGCGAGCAGTATCGCTCATTGAACTGGCCAAAATAGGG  
ACCTTGAGAAGGAAGGGAGCTCGGCTTCTCTGAGTGCTTCGCGGTGCACCCCTGTCTCGGAAGGTACCTCTCATGT  
ACCGGCTCCACAAACGCTTCAAGCCTCTGGAGTTGGAGCGGGCTTACAGTGAATAGAACACTGCAGGCTCAGA  
TCCGAACCTGACCCTGTCTGACCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGCTTGGGCTCCTCTGCTCCTTTCA  
CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCAAGAGCAGCACACCTTCTCCTGTGCAGATGGG  
CTCCCAAGTGCCCACTACAGGGGCTAGCAGGGCGGACGTGGTGATCGTGTGGAGACTGCCCTGGAGCAGTCA  
ATCGGCGTATCAGCCCCGCTGCGCTTCCAGAAGCAGCGACTGTCAACGGGTATCGGCGCTTGACCCAGCAC  
GGGCGATGGAGTACACCCCTGGACCTGCTGTGGAATGTGTGACACAGCGTGGGCACCGCGGGCCCTGGCTGGCA  
GGGTGAGCTGCTGCGGCCACTGAGCCGGGTGGAATCCTACCTATGCCCTATGTCTCACTGAGGCCACCCGAGTGC  
AGCTGGCTGCTGCACTCTGTGGTGGCTGAACTGTCTGAGCCCGGCTTCTCTGAGGCGTTTGCAGCCATATGCC  
TGGAGCCACGAGAACTGCATTGCTCAACCTGTGCTGGTCTACGGGCCACGAGAAGGTGGCCCTGGAGCTCCAG  
ACCCATTCTTTGGGTGGAAGCTGCAGCAGCGGAGTTAGAGCGAGGCTACCTTGGGACGAGGCTGGCCTGGCTCG  
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGACGCTGTCTCAAGAAGCACCCCTGTGGAACACTCTCT  
TCTTCTTACCACCGTGTGGACAAAGCCTGGGCCGGAAGTCTCAACCGCTGTGCGCATGAATGCCATCTCTGCT  
GGCAGGCTCTTTTCCAGTCCATTTCCAGGAGTTCAATCTGCTGCCCTGTCAACACAGAGATCAACCCAGCGCCCC  
CGGGGCTGGCCCTGACCCCGCTCCCTCCTGCTGCTGACCCCTCCGGGGGGCTCTTATAGGGGGAGATTG  
ACCGGCAAGTTCTGCGGAGGCTGCTTCTACAACGCTGACTTACCTGGCCGCGAGCCCGCTGCGAGGTGA  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGATGTTTCTCCTCGGTTCTCAGGGCTCC  
ACCTCTTTTGGGCCGTAGAGCCAGGGCTGGTGCAAGATTCTCCTGCGAGACTGCAGCCACCGCTCAGTGAAG  
AACTCTACACCGCTGCCGCTCAGCAACCTGGAGGGGCTAGGGGGCGCTGCCAGCTGGCTATGGCTCTCTTG  
AGCAGGAGCAGCCATAAGCACTAGCCCGCTGGGGGCCCTAACTCATTACTTTCTTTGTCTGCTCCAGCC  
CAGGAAGGCCAAGCAAGATGTGGACAGATAGAGAAATGTTGCTGATTTTAAATATGAAAATGTTATTAA  
ACATGTCTTCTGCG

CCAGGCTCTCTG

## FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPDSSRARLD  
 QSDDFKPRIVPYYYRDPNKPYPKVLRTYIQTTELGSRRLLVAVLTSRATLSTLAVAVNRTV  
 AHHPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY  
 VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG  
 DILSARDEWLGRCLIDSLGVGCVSQHQGQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
 GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV  
 LGWDYFTEQHTFSCADGAPKCPLOGASRADVGDALETALEQLNRRYQPRLRQKQRLNNGYR  
 RFDPARGMEYTLDLLLECVTQRGHRRLARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL  
 VAEAAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAABLERYPG  
 TRLAWLAVRAEAPSQVRLMDVSVKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFPP  
 VHFQEFNPALSPQRSPPGPPGAGDPDPPSPGADPSRGAPIGGRFDRQASAEQCFYNADYLAA  
 RARLAGELAGQEEEEALEGLEVMVDVFLRFSGHLHFRFAVEPGLVQKFSLRDCSPRLSEELYHR  
 CRLSNLEGLGGRAQLAMALFEQEQUANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
 399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
 558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250



## FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLSAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLKKDPSQPPYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPQQGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFN  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

### **Signal sequence:**

amino acids 1-33

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250



[illegible]

100  
 90  
 80  
 70  
 60  
 50  
 40  
 30  
 20  
 10  
 0

Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38



## **FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624  
><subunit 1 of 1, 310 aa, 1 stop  
><MW: 35020, pI: 7.90, NX(S/T): 3  
MALRRPPRLRLCARLPDFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSCLKIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVT PVC RVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGG  
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-30

#### **Transmembrane domain:**

amino acids 243-263

#### **N-glycosylation sites.**

amino acids 104-107, 192-195

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

#### **Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

#### **Tyrosine kinase phosphorylation site.**

amino acids 69-77

#### **N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267